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OM protein - protein search, using sw model

Run on: February 20, 2003, 10:04:02 ; Search time 19.8095 Seconds
(without alignments)
47.529 Million cell updates/sec

Title: US-09-776-781-6
Perfect score: 158
Sequence: 1 MAPSSSTKTKQLQLHLLKQLMILGINNY 32

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A.COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B.COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS.COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	152	96.2	96	1	US-08-160-376A-5
2	152	96.2	96	1	US-08-389-487-8
3	152	96.2	134	6	5496924-55
4	147	93.0	50	1	US-08-127-351-13
5	147	93.0	50	1	US-08-480-367B-13
6	147	93.0	50	1	US-08-487-221A-13
7	147	93.0	50	1	US-08-480-370-13
8	147	93.0	88	4	US-08-817-787-15
9	147	93.0	133	1	US-07-800-366-1
10	147	93.0	133	1	US-08-354-456A-5
11	147	93.0	133	1	US-08-225-224-3
12	147	93.0	133	1	US-08-318-193-89
13	147	93.0	133	1	US-08-284-393B-1
14	147	93.0	133	1	US-08-284-393B-2
15	147	93.0	133	1	US-08-284-393B-3
16	147	93.0	133	1	US-08-734-471-1
17	147	93.0	133	3	US-08-722-258-3
18	147	93.0	133	4	US-08-817-787-13
19	147	93.0	133	4	US-09-310-026-1
20	147	93.0	133	5	PCT-US95-04468-3
21	147	93.0	133	5	PCT-US95-08950-1
22	147	93.0	133	5	PCT-US95-08950-2
23	147	93.0	133	5	PCT-US95-08950-3
24	147	93.0	133	6	5210029-1
25	147	93.0	133	6	5256769-1
26	147	93.0	133	6	5464939-2
27	147	93.0	153	3	US-09-012-366-3

28	147	93.0	153	4	US-08-759-628-8	Sequence 8, Appli
29	147	93.0	153	4	US-09-522-217-111	Sequence 111, App
30	147	93.0	153	6	5314995-7	Patent No. 5314995
31	147	93.0	157	4	US-08-818-562-2	Sequence 2, Appli
32	147	93.0	157	4	US-09-628-445-2	Sequence 2, Appli
33	147	93.0	478	3	US-08-155-888-2	Sequence 2, Appli
34	147	93.0	504	1	US-07-932-915-2	Sequence 2, Appli
35	147	93.0	504	5	PCT-US91-05826-2	Sequence 2, Appli
36	145	91.8	31	4	US-09-116-594-2	Sequence 2, Appli
37	144	91.1	251	3	US-08-875-811-59	Sequence 59, Appl
38	144	91.1	254	3	US-08-875-811-61	Sequence 61, Appl
39	143	90.5	133	1	US-08-354-456A-6	Sequence 6, Appli
40	132.5	83.9	127	3	US-08-806-121B-3	Sequence 3, Appli
41	132.5	83.9	127	4	US-09-443-061-3	Sequence 3, Appli
42	100	63.3	141	4	US-08-930-917A-18	Sequence 18, Appl
43	96	60.8	21	4	US-09-570-921-63	Sequence 63, Appl
44	96	60.8	21	4	US-09-570-921-68	Sequence 68, Appl
45	72	45.6	135	2	US-08-383-621-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-08-160-376A-5
; Sequence 5, Application US/08160376A
; Patent No. 5473049
; GENERAL INFORMATION:
; APPLICANT: Obermeier, Ranier
; APPLICANT: Gerl, Martin
; APPLICANT: Ludwig, Jurgen
; APPLICANT: Sabel, Walter
; TITLE OF INVENTION: Process For Obtaining Proinsulin
; TITLE OF INVENTION: Possessing Correctly Linked
; TITLE OF INVENTION: Cystine Bridges
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenneth A. Genoni, Esq.
; STREET: Rt. 202-206 No. 5473049th/P.O. Box 2500
; CITY: Somerville
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 08876-1258
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
; COMPUTER: IBM 386
; OPERATING SYSTEM: WINDOWS 3.1
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/160.376A
; FILING DATE: December 1, 1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GE P 4240420.7
; FILING DATE: December 2, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Barbara V. Maurer, Esq.
; REGISTRATION NUMBER: 31,287
; REFERENCE/DOCKET NUMBER: HOE 92/F 384
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 231-4079
; TELEFAX: (908) 231-2255
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 96 Amino Acids
; TYPE: Amino Acid (AA)
; TOPOLOGY: not relevant
; US-08-160-376A-5

Query Match 96.2%; Score 152; DB 1; Length 96;
Best Local Similarity 96.9%; Pred. No. 4.1e-16;
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAPTSSSTKKTQLEHLLKLMILGINNY 32
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Db 1 MAPTSSSTKKTQLEHLLDLMILGINNY 32

RESULT 2

US-08-389-487-8
; Sequence 8, Application US/08389487
; Patent No. 5663291
; GENERAL INFORMATION:
; APPLICANT: Obermeier, Rainer
; APPLICANT: Gerl, Martin
; APPLICANT: Ludwig, Jurgen
; APPLICANT: Sabel, Walter
; TITLE OF INVENTION: Process for Obtaining Insulin Having
; TITLE OF INVENTION: Correctly Linked Cysteine Bridges
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States of America
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/389,487
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Einaudi, Carol P.
; REGISTRATION NUMBER: 32,220
; REFERENCE/DOCKET NUMBER: 02481.1424-00000
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 96 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-389-487-8

Query Match 96.2%; Score 152; DB 1; Length 96;
Best Local Similarity 96.9%; Pred. No. 4.1e-16;
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAPTSSSTKKTQLEHLLKLMILGINNY 32
|||||
Db 1 MAPTSSSTKKTQLEHLLDLMILGINNY 32

RESULT 3

5496924-55
; Patent No. 5496924
; APPLICANT: HABERMANN, PAUL; WENGEMAYER, FRIEDRICH
; TITLE OF INVENTION: FUSION PROTEIN COMPRISING AN
; INTERLEUKIN-2 FRAGMENT BALLAST PORTION
; NUMBER OF SEQUENCES: 56
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/194,545
; FILING DATE: 28-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 377,313
; FILING DATE: 10-JUL-1989
; APPLICATION NUMBER: 934,910

; FILING DATE: 25-NOV-1986
; APPLICATION NUMBER: 943,804
; FILING DATE: 19-DEC-1986
; SEQ ID NO: 55
; LENGTH: 134
5496924-55

Query Match 96.2%; Score 152; DB 6; Length 134;
Best Local Similarity 96.9%; Pred. No. 6.2e-16;
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAPTSSSTKKTQLEHLLKLMILGINNY 32
|||||
Db 1 MAPTSSSTKKTQLEHLLDLMILGINNY 32

RESULT 4

US-08-127-351-13
; Sequence 13, Application US/08127351
; Patent No. 5449761
; GENERAL INFORMATION:
; APPLICANT: BELINKA JR, BENJAMIN A.
; APPLICANT: COUGHLIN, DANIEL J.
; APPLICANT: ALVAREZ, VERNON L.
; APPLICANT: WOOD, RICHARD
; TITLE OF INVENTION: METAL-BINDING TARGETED POLYPEPTIDE
; TITLE OF INVENTION: CONSTRUCTS
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER &
; ADDRESSEE: NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/127,351
; FILING DATE: 28-SEP-1993
; CLASSIFICATION: 534
; ATTORNEY/AGENT INFORMATION:
; NAME: Villacorta, Gilberto M.
; REGISTRATION NUMBER: 34,038
; REFERENCE/DOCKET NUMBER: 4980-004-44
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-127-351-13

Query Match 93.0%; Score 147; DB 1; Length 50;
Best Local Similarity 96.8%; Pred. No. 1.1e-15;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLEHLLKLMILGINNY 32
|||||
Db 1 APTSSSTKKTQLEHLLDLMILGINNY 31

RESULT 5

US-08-480-367B-13

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; Sequence 13, Application US/08480367B
; Patent No. 5578288
; GENERAL INFORMATION:
; APPLICANT: BELINKA JR, BENJAMIN A.
; APPLICANT: COUGHLIN, DANIEL J.
; APPLICANT: ALVAREZ, VERNON L.
; APPLICANT: WOOD, RICHARD
; TITLE OF INVENTION: METAL-BINDING TARGETED POLYPEPTIDE
; TITLE OF INVENTION: CONSTRUCTS
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LOWE, PRICE, LeBLANC & BECKER
; STREET: 99 Canal Center Plaza, Suite 300
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,367B
; FILING DATE: 07-06-95
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Villacorta, Gilberto M.
; REGISTRATION NUMBER: 34,038
; REFERENCE/DOCKET NUMBER: 2654-002A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 684-1111
; TELEFAX: (703) 684-1124
; TELEX:
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-480-367B-13

Query Match 93.0%; Score 147; DB 1; Length 5
Best Local Similarity 96.8%; Pred. No. 1.le-15;
Matches 30; Conservative 0; Mismatches 1; Indels 1

QY 2 APTSSSTKKTQLEHLHLKLQWLINGNNY 32
| | | | | | | | | | | | | | | | | |
Db 1 APTSSSTKKTQLEHLHLKLQWLINGNNY 31

RESULT 6
US-08-487-221A-13
; Sequence 13, Application US/08487221A
; Patent No. 5593656
; GENERAL INFORMATION:
; APPLICANT: BELINKA JR, BENJAMIN A.
; APPLICANT: COUGHLIN, DANIEL J.
; APPLICANT: ALVAREZ, VERNON L.
; APPLICANT: WOOD, RICHARD
; TITLE OF INVENTION: METAL-BINDING TARGETED POLYPEPTIDE
; TITLE OF INVENTION: CONSTRUCTS
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBOLON, SPIVAK, McCLELLAND, MAIER &
; ADDRESS: NEUSTADT, P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-480-370-13

Query Match 93.0%; Score 147; DB 1; Length 50;
Best Local Similarity 96.8%; Pred. No. 1.1e-15;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 APTSSSTKTKQLQLEHLLLDLQMLNGINNY 32
DB 1 APTSSSTKTKQLQLEHLLLDLQMLNGINNY 31

RESULT 8
US-08-817-787-15
Sequence 15 Application US/08817787
Patent No. 6294353
GENERAL INFORMATION:
APPLICANT: Pack, Peter
APPLICANT: Lupas, Andrei
TITLE OF INVENTION: TARGETED HETERO-ASSOCIATION OF
RECOMBINANT PROTEINS TO MULTI-FUNCTIONAL COMPLEXES
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10020

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,787
FILING DATE: 23-SEP-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP95/04117
FILING DATE:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94 11 6558.1
FILING DATE: 20-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Halsey Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/1
TELEPHONE: 212-596-9000
TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 88 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-817-787-15

Query Match 93.0%; Score 147; DB 4; Length 88;
Best Local Similarity 96.8%; Pred. No. 2.2e-15;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 APTSSSTKTKQLQLEHLLLDLQMLNGINNY 32
DB 1 APTSSSTKTKQLQLEHLLLDLQMLNGINNY 31

Db 3 APTSSSTKTKQLQLEHLLLDLQMLNGINNY 33

RESULT 9
US-07-800-366-1
Sequence 1, Application US/07800366
Patent No. 5250296
GENERAL INFORMATION:
APPLICANT: OOTSU, Koichiro
TITLE OF INVENTION: IMMUNOSTIMULANT AGENT CONTAINING
INTERLEUKIN-2 AND 5'-DEOXY-5-FLUOROURIDINE
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
ADDRESSEE: CUSHMAN
STREET: 130 Water Street
CITY: Boston
STATE: Massachusetts
COUNTRY: US
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/800,366
FILING DATE: 19911127
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Castle, Donald R
REGISTRATION NUMBER: 24,220
REFERENCE/DOCKET NUMBER: 41417(281)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
TELEFAX: (617)523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 133 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-800-366-1

Query Match 93.0%; Score 147; DB 1; Length 133;
Best Local Similarity 96.8%; Pred. No. 3.6e-15;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 APTSSSTKTKQLQLEHLLLDLQMLNGINNY 32
DB 1 APTSSSTKTKQLQLEHLLLDLQMLNGINNY 31

RESULT 10
US-08-354-456A-5
Sequence 5, Application US/08354456A
Patent No. 5567611
GENERAL INFORMATION:
APPLICANT: Ralph, Peter
APPLICANT: Martin, George
APPLICANT: Platek, Michael
APPLICANT: Larrick, James W.
TITLE OF INVENTION: Multifunctional M-CSF Proteins and Genes Encoding
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHIRON CORPORATION
STREET: Intellectual Property - R440, P.O. Box 8097
CITY: Emeryville
STATE: California
COUNTRY: U.S.A.
ZIP: 94662-8097


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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/354,456A
; FILING DATE: 12-DEC-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/995,338
; FILING DATE: 21-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: McGarrigle Jr., Philip L.
; REGISTRATION NUMBER: 31,395
; REFERENCE/DOCKET NUMBER: 750.003/32387
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2718
; TELEFAX: (510) 655-3542
; TELEX: n/a
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 133 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-354-456A-5

Query Match          93.0%; Score 147; DB 1; Length 133;
Best Local Similarity 96.8%; Pred. No. 3.6e-15;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLQLEHLLKLQMLNGINNY 32
DB 1 APTSSSTKKTQLQLEHLLLDLQMLNGINNY 31

RESULT 11
US-08-225-224-3
; Sequence 3, Application US/08225224
; Patent No. 5635599
; GENERAL INFORMATION:
; APPLICANT: PASTAN, Ira
; TITLE OF INVENTION: CIRCULARLY PERMUTATED LIGANDS AND
; TITLE OF INVENTION: CIRCULARLY PERMUTATED FUSION PROTEINS
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/225,224
; FILING DATE: 8-APR-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen L.
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 15280-193
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 3:
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 133 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..133
; OTHER INFORMATION: /label= IL2
; US-08-225-224-3

Query Match          93.0%; Score 147; DB 1; Length 133;
Best Local Similarity 96.8%; Pred. No. 3.6e-15;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLQLEHLLKLQMLNGINNY 32
DB 1 APTSSSTKKTQLQLEHLLLDLQMLNGINNY 31

RESULT 12
US-08-318-193-89
; Sequence 89, Application US/08318193
; Patent No. 5641663
; GENERAL INFORMATION:
; APPLICANT: GARVIN, Robert T.
; APPLICANT: MALEK, Lawrence T.
; TITLE OF INVENTION: AN EXPRESSION SYSTEM FOR THE SECRETION
; TITLE OF INVENTION: OF BIOACTIVE HUMAN GRANULOCYTE MACROPHAGE COLONY
; TITLE OF INVENTION: STIMULATING FACTOR (GM-CSF) AND OTHER HETEROLOGOUS
; TITLE OF INVENTION: PROTEINS FROM STREPTOMYCES
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,193
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,314
; FILING DATE:
; APPLICATION NUMBER: US 07/224,568
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 18740/116 CACO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 89:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 133 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-318-193-89

Query Match          93.0%; Score 147; DB 1; Length 133;
Best Local Similarity 96.8%; Pred. No. 3.6e-15;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Query Match 93.0%; Score 147; DB 1; Length 133;
 Best Local Similarity 96.8%; Pred. No. 3.6e-15;
 Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 APTSSSTKKTQLQLEHLLKLQMLINGINNY 32
 |||||
 Db 1 APTSSSTKKTQLQLEHLLKLQMLINGINNY 31

Search completed: February 20, 2003, 10:08:10
 Job time : 20.8095 secs

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GenCore version 5.1.1.3
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OM protein - protein search, using sw model

Run on: February 20, 2003, 10:00:37 ; Search time 30.9841 Seconds
(without alignments)
137.619 Million cell updates/sec

Title: US-09-776-781-6

Perfect score: 158

Sequence: 1 MAPTSSSTKKYQLQLEHLLKLQMLINGINNY 32

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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- 2: /SID2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
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- 12: /SID2/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*
- 13: /SID2/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*
- 14: /SID2/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:*
- 15: /SID2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*
- 16: /SID2/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:*
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- 19: /SID2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
- 20: /SID2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
- 21: /SID2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
- 22: /SID2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
- 23: /SID2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	158	100.0	32	23	Interleukin-2 pept
2	154	97.5	134	8	Sequence of segmen
3	153	96.8	31	23	Interleukin-2 pept
4	153	96.8	133	21	Amino acid sequenc
5	152	96.2	58	12	Human interleukin-
6	152	96.2	60	11	Human IL-2 N-termi
7	152	96.2	60	15	Human Interleukin-
8	152	96.2	96	15	Human pro-insulin
9	152	96.2	96	16	Fusion protein con
10	152	96.2	133	13	Interleukin-2 used

11	152	96.2	134	5	AA040050	Sequence of an int
12	152	96.2	134	6	AA050053	Sequence I of new
13	152	96.2	134	6	AA050855	Sequence encoded b
14	152	96.2	134	7	AA061102	Sequence of human
15	152	96.2	134	8	AA070585	Sequence of mature
16	152	96.2	134	11	AA05267	Sequence of natura
17	152	96.2	134	11	AA05266	Sequence of natura
18	152	96.2	134	11	AA05240	Human interleukin
19	152	96.2	136	20	AA049917	tabl. Synthetic.
20	152	96.2	143	15	AA050932	Recombinant Interl
21	152	96.2	149	11	AA07265	Recombinant Interl
22	152	96.2	149	11	AA07266	Recombinant Interl
23	152	96.2	149	11	AA07267	Recombinant Interl
24	152	96.2	149	11	AA07269	Recombinant Interl
25	152	96.2	149	11	AA07148	Recombinant Interl
26	152	96.2	149	11	AA07149	Recombinant Interl
27	152	96.2	149	11	AA07150	Recombinant Interl
28	152	96.2	149	11	AA07261	Recombinant Interl
29	152	96.2	149	11	AA07262	Recombinant Interl
30	152	96.2	149	11	AA07263	Recombinant Interl
31	152	96.2	149	11	AA07264	Recombinant Interl
32	152	96.2	172	10	AA094809	Human interleukin
33	152	96.2	201	11	AA06839	Human IL-2 N-termi
34	152	96.2	255	6	AA050305	Fused antibody rec
35	152	96.2	273	6	AA050887	Conjugate of inter
36	152	96.2	273	6	AA050310	Interferon-gamma a
37	150	94.9	133	21	AA053829	Amino acid sequenc
38	149	94.3	65	10	AA091032	Human interleukin-
39	149	94.3	133	21	AA053828	Amino acid sequenc
40	149	94.3	149	11	AA07146	Recombinant Interl
41	149	94.3	149	11	AA07268	Recombinant Interl
42	149	94.3	149	11	AA07255	Recombinant Interl
43	149	94.3	149	11	AA07256	Recombinant Interl
44	149	94.3	149	11	AA07257	Recombinant Interl
45	149	94.3	149	11	AA07258	Recombinant Interl

ALIGNMENTS

RESULT 1

ABB79534

ID ABB79534 standard; Peptide; 32 AA.

AC ABB79534;

XX

XX

DT 23-SEP-2002 (first entry)

XX

DE Interleukin-2 peptide IPI31 (D20K).

XX

KW IPI31; interleukin-2; human; gene; gene therapy; mutant; mutein.

XX

OS Homo sapiens.

OS Synthetic.

XX

XX

Key Location/Qualifiers

FT Misc-difference 21

FT /note= *wild-type Asp substituted by Lys*

XX

PN US2002044935-A1.

XX

PD 18-APR-2002.

XX

PF 06-FEB-2001; 2001US-0776781.

XX

PR 16-JUL-1998; 98US-0116594.

XX

PR 12-SEP-2000; 2000US-0660465.

XX

PA (INSP) INST PASTEUR.

XX

PI Theze J, Eckenberg R, Moreau J, Goldberg M, Rose T, Alzari P;

PI Mazie J;

XX

DR WPI: 2002-546505/58.
 DR N-PSDB; ABN84295.
 XX New peptides derived from Interleukin 2 designated IP130 and IP131 are
 PT useful as therapeutic agents in the treatment of patients deficient in
 PT IL-2 activity -
 XX
 PS Claim 18; Page 2; 53pp; English.
 XX
 CC The present sequence is the protein sequence for IP131 D20K. The
 CC sequence is based on the human interleukin-2 (IL-2) peptide IP130
 CC (see ABN84292) by the addition of a C-terminal Tyr residue, and
 CC substitution of the native Asp-20 residue by Lys. Asp-20 is
 CC located in a region of IL-2 that directly influences interaction of
 CC the cytokine with its receptor (IL-2R). An antibody that binds to
 CC the peptide is claimed, and is preferably an antibody produced by
 CC hybridoma H2-8 (CNCM No. I-2338). A claimed method of detecting
 CC the presence or activity of involves contacting a sample with
 CC IP131 D20K, and detecting whether binding occurs. A claimed method
 CC for inhibiting IL-2R activity involves contacting IL-2R with the
 CC peptide. A claimed method for inducing IL-2 activity in a patient
 CC comprises administering IP131 D20K to the patient. A vector
 CC containing DNA encoding the peptide is claimed, and is used in a
 CC claimed method for treating a patient deficient in IL-2 activity.
 CC Also claimed are peptides corresponding to IP131 D20K but
 CC containing conservative amino acid substitutions, i.e. change of
 CC non-polar R-groups but other non-polar R-groups, change of
 CC uncharged polar R-groups by other uncharged polar R-groups,
 CC substitution of Arg by Lys, Asp by Glu, Thr by Ser, or Asn by
 CC Gln, and vice versa. The peptide induces SHC phosphorylation or
 CC induction of the SHC/MAPK pathway. Antibodies specific for the
 CC peptide are useful for treatment or prevention of undesirable
 CC immune reactions such as graft rejection, or autoimmune disorders
 CC such as rheumatoid arthritis.
 XX
 SQ Sequence 32 AA;
 Query Match 100.0%; Score 158; DB 23; Length 32;
 Best Local Similarity 100.0%; Pred. No. 2.7e-15;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAPSSSTKTKQLQLEHLLKIQMLINGINNY 32
 DB 1 MAPSSSTKTKQLQLEHLLKIQMLINGINNY 32
 RESULT 2
 AAP70573
 ID AAP70573 standard; Protein; 134 AA.
 AC AAP70573;
 XX
 XX 27-MAY-1991 (first entry)
 DT
 XX Sequence of segments A-F of interleukin-2 (IL-2).
 DE
 XX Interleukin-2 fusion protein; ballast fragment.
 KW
 XX DE3636903-A.
 PN
 XX 02-JUL-1987.
 PD
 XX 30-OCT-1986; 86DE-3636903.
 PF
 XX 21-DEC-1985; 85DE-3545565.
 PR
 XX 30-OCT-1986; 86DE-3636903.
 XX
 XX (FARH) HOECHST AG.
 PA
 XX Habermann P;
 PI
 XX WPI; 1987-186353/27.
 DR
 XX N-PSDB; AAN70921.

XX New fusion protein contg. small interleukin 2 ballast fragments -
 PT allowing control of product solubility, and corresp. genes,
 PT vectors and transformed host cells
 XX
 PS Disclosure; pp8-9; 22pp; German.
 XX
 CC The inventors claim a novel fusion protein which has a C- or N-
 CC terminal portion corresponding essentially to the AA sequence of
 CC interleukin-2 (IL-2) but contg. less than 100 AAs. The IL-2 sequence
 CC is coded for by 1,2 or 3 of the A-F segments of the IL-2 gene having
 CC the formula: (EcoRI)-A-PstI-B-MluI-C-XbaI-D-SacI-E-PvuI-F-(SalI),
 CC for example, the sequence in AAN70921. The segments are joined in any
 CC appropriate sequence and opt. connected by usual adaptors or linkers.
 XX
 SQ Sequence 134 AA;
 Query Match 97.5%; Score 154; DB 8; Length 134;
 Best Local Similarity 96.9%; Pred. No. 4.7e-14;
 Matches 31; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAPSSSTKTKQLQLEHLLKIQMLINGINNY 32
 DB 1 MAPSSSTKTKQLQLEHLLKIQMLINGINNY 32
 RESULT 3
 ABB79535
 ID ABB79535 standard; Peptide; 31 AA.
 XX
 AC ABB79535;
 XX
 XX 23-SEP-2002 (first entry)
 DT
 XX Interleukin-2 peptide IP131 (D20K).
 DE
 XX IP131; Interleukin-2; human; gene; gene therapy; mutant; mutein.
 KW
 XX Homo sapiens.
 OS
 XX Synthetic.
 XX
 XX Key Location/Qualifiers
 FT Misc-difference 20
 FT /note= "wild-type Asp substituted by Lys"
 XX
 XX US2002044935-A1.
 XX
 XX 18-APR-2002.
 PD
 XX 06-FEB-2001; 2001US-0776781.
 PF
 XX 16-JUL-1998; 98US-0116594.
 PR
 XX 12-SEP-2000; 2000US-0660465.
 XX
 XX (INSP) INST PASTEUR.
 PA
 XX Theze J, Eckenberg R, Moreau J, Goldberg M, Rose T, Alzari P;
 PI Mazie J;
 PI
 XX WPI; 2002-546505/58.
 DR
 XX N-PSDB; ABN84296.
 DR
 XX New peptides derived from Interleukin 2 designated IP130 and IP131 are
 PT useful as therapeutic agents in the treatment of patients deficient in
 PT IL-2 activity -
 XX
 PS Claim 18; Page -; 53pp; English.
 XX
 CC The present sequence is the protein sequence for IP131 D20K. The
 CC sequence is based on the human interleukin-2 (IL-2) peptide IP130
 CC (see ABN84292) by the addition of a C-terminal Tyr residue, and
 CC substitution of the native Asp-20 residue by Lys. Asp-20 is
 CC located in a region of IL-2 that directly influences interaction of
 CC the cytokine with its receptor (IL-2R). An antibody that binds to
 CC the peptide is claimed, and is preferably an antibody produced by
 CC hybridoma H2-8 (CNCM No. I-2338). A claimed method of detecting
 CC the presence or activity of involves contacting a sample with
 CC IP131 D20K, and detecting whether binding occurs. A claimed method
 CC for inhibiting IL-2R activity involves contacting IL-2R with the
 CC peptide. A claimed method for inducing IL-2 activity in a patient
 CC comprises administering IP131 D20K to the patient. A vector
 CC containing DNA encoding the peptide is claimed, and is used in a
 CC claimed method for treating a patient deficient in IL-2 activity.
 CC Also claimed are peptides corresponding to IP131 D20K but
 CC containing conservative amino acid substitutions, i.e. change of
 CC non-polar R-groups but other non-polar R-groups, change of
 CC uncharged polar R-groups by other uncharged polar R-groups,
 CC substitution of Arg by Lys, Asp by Glu, Thr by Ser, or Asn by
 CC Gln, and vice versa. The peptide induces SHC phosphorylation or
 CC induction of the SHC/MAPK pathway. Antibodies specific for the
 CC peptide are useful for treatment or prevention of undesirable
 CC immune reactions such as graft rejection, or autoimmune disorders
 CC such as rheumatoid arthritis.

```

XX Example 5; Page -: 80pp; English.
XX
XX
CC AAY53822-66 represent human interleukin-2 (IL-2) mutants, where human
CC IL-2 has been substituted at one of positions 20, 88 or 126. Wild-type
CC IL-2, when used in cancer treatment, has adverse side effects. The
CC toxicities associated with IL-2 therapy include severe fever, nausea,
CC vomiting, vascular leak and serious hypotension. The mutants described
CC in this invention have reduced toxicity and are better tolerated. It is
CC the mediation of IL-2 through natural killer cells which causes the
CC toxicity whereas the efficacy is mediated by the direct activation of T
CC cells. The mutants preferentially activate T cells over natural killer
CC cells. IL-2 mutants may be used for treating a mammal afflicted with an
CC IL-2 treatable condition. The condition may be one of the following:
CC HIV, cancer including renal carcinoma and malignant melanoma, autoimmune
CC disease, infectious disease, immune deficiency including SCID or other
CC therapeutic application requiring general stimulation of the immune
CC system. Other potential uses include treatment of infectious diseases
CC such as tuberculosis and as an adjuvant in cancer vaccine strategy. The
CC DNA sequences encoding the IL-2 mutant may be used in gene therapy
CC applications in those diseases in which IL-2 is expected to provide an
CC effective therapy due to its T cell activity.
CC note: this sequence does not appear in the specification; it was created
CC using information provided and the wild type IL-2 sequence (see
CC AAY53821).
XX
XX SQ Sequence 133 AA;
Query Match 96.8%; Score 153; DB 21; Length 133;
Best Local Similarity 100.0%; Pred. NO. 6.5e-14;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps
QY 2 APRSSSTKTKTQLQLEHLLKLQMILINGINNY 32
DB 1 APRSSSTKTKTQLQLEHLLKLQMILINGINNY 31
RESULT 5
AAR11015
ID AAR11015 standard; Peptide; 58 AA.
XX AC AAR11015;
XX 13-MAY-1991 (first entry)
XX Human interleukin-2-derived stabiliser peptide.
DE Interleukin-2; IL-2; gag 24; gp 41; gp 36; HIV detection.
KW Homo sapiens.
OS EP41673-A.
PN 13-MAR-1991.
PD 02-AUG-1990; 90EP-0202108.
XX PF 03-AUG-1989; 89CU-0000149.
PR (INGE-) CENT ING GENETICA.
XX Novoa Perez LI, Machado Lahera JA, Fernandez Maso JR;
PI Benitez Fuentes JV, Narcandi Diaz RE, Rodriguez Reinoso JL;
PI Estrada Garcia MP, Garcia Suarez J, Herrera Martinez LS;
XX WPI; 1991-075192/11.
DR N-PSDB; AAQ10898.
XX Method for expressing heterologous proteins - as fusion protein,
PT using vector contg. stabilising sequence
XX Claim 2; Page 10; 18pp; English.
XX PS
XX
```

CC The sequence corresponds to the first 58 amino acid residues of
 CC human IL-2. It forms part of a fusion protein, linked to a
 CC heterologous protein. The heterologous protein is preferably gag 24
 CC or a fragment of gp 41 of HIV-1 or it is a fragment of gp 36 of
 CC HIV-2. Such fusion proteins can be used to detect antibodies to
 CC these proteins. See also AAQ10899-Q10903.

XX Sequence 58 AA;

Query Match 96.2%; Score 152; DB 12; Length 58;
 Best Local Similarity 96.9%; Pred. No. 3.6e-14;
 Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MAPSSSTKKTQLQLEHLLKLLQMLINGINNY 32
 |||||

Db 1 MAPSSSTKKTQLQLEHLLKLLQMLINGINNY 32
 |||||

RESULT 6

AA06838
 ID AAR06838 standard; protein; 60 AA.

XX AAR06838;

XX 14-JAN-1991 (first entry)

XX Human IL-2 N-terminal transcript of plasmid pTl3S.

XX Bovine tuberculosis; Interleukin-2; IL-2; plasmid pTl3S.

XX Mycobacterium bovis.

XX JP02195895-A.

XX 02-AUG-1990.

XX 24-JAN-1989; 89JP-0013270.

XX 24-JAN-1989; 89JP-0013270.

XX (AJIN) AJINOMOTO KK.

XX WPI; 1990-278851/37.

DR N-PSDB; AAQ05976.

XX BCG bacteria derived immuno:protein MPB70 - can be used as
 PT diagnostic agent used to determine bovine tuberculosis.

XX Disclosure; Fig 2; 11pp; Japanese.

XX Immunoprotein MPB 70 encoding sequence may be incorporated into
 CC plasmid pTl3S with an N-terminal fragment of human IL-2. The plasmid
 CC may be used to transform an expression system giving a fusion
 CC protein which may be used as a diagnostic agent for bovine
 CC tuberculosis infection.

XX Sequence 60 AA;

Query Match 96.2%; Score 152; DB 11; Length 60;
 Best Local Similarity 96.9%; Pred. No. 3.8e-14;
 Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MAPSSSTKKTQLQLEHLLKLLQMLINGINNY 32
 |||||

Db 1 MAPSSSTKKTQLQLEHLLKLLQMLINGINNY 32
 |||||

RESULT 7

AA48245

ID AAR48245 standard; protein; 60 AA.

XX AC

XX AAR48245;

XX

DT 12-JUL-1994 (first entry)

XX Human Interleukin-2.

XX non-coding region; coding region; resonance; interaction; IL-2;
 KW optimisation; degenerate sequence; plasmid pTl3Snc; pT9-11;
 KW gene expression; regulation; recombinant protein production;
 KW interleukin-2; interleukin-6.

XX Homo sapiens.

XX FR2692594-A.

XX 24-DEC-1993.

XX 22-JUN-1992; 92FR-0007571.

XX 22-JUN-1992; 92FR-0007571.

XX (PERE/) PEREZ J.

XX Perez J;

XX WPI; 1994-028256/04.

XX N-PSDB; AAQ55629; AAQ55630.

XX Application of optimised gene expression - for scientific,
 PT industrial and therapeutic purposes

XX Disclosure; Fig 28 and Fig 29; 110pp; French.

XX Resonances between coding and non-coding regions were measured for
 CC the native human IL-2 gene in plasmid pT911 (see AAQ55630) and a
 CC synthetic IL-2 gene (AAQ55629) in which alternative, degenerate
 CC codons were used in order to introduce additional restriction
 CC sites. It was found that the degenerate changes greatly upset the
 CC "natural order" between coding and non-coding regions; as a result,
 CC the amount of protein expressed by the degenerate gene is likely to
 CC be adversely affected. The inventors have proposed an "optimised"
 CC IL-2 gene with the aim of increasing the amount of protein expressed
 CC by the gene. (N.B. the sequence is also described as
 CC interleukin-6).

XX Sequence 60 AA;

Query Match 96.2%; Score 152; DB 15; Length 60;
 Best Local Similarity 96.9%; Pred. No. 3.8e-14;
 Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MAPSSSTKKTQLQLEHLLKLLQMLINGINNY 32
 |||||

Db 1 MAPSSSTKKTQLQLEHLLKLLQMLINGINNY 32
 |||||

RESULT 8

AA68899

ID AAR68899 standard; peptide; 96 AA.

XX AAR68899;

XX 02-MAR-1995 (first entry)

XX Human pro-insulin 2.

XX Pro-insulin; A-chain; B-chain; C-chain; disulphide;
 KW mercaptan; chaotropic agent.

XX Homo sapiens.

XX EP600372-A.

XX 08-JUN-1994.

XX

PF 25-NOV-1993; 93EP-0118993.
 XX
 PR 02-DEC-1992; 92DE-4240420.
 XX
 PA (FARH) HOECHST AG.
 XX
 PI Gerl M, Ludwig J, Obermeier R, Sabel W;
 XX
 DR WPI; 1994-177718/22.
 XX

PT Prodn. of pro-insulin with correct di-sulphide bridges - by
 PT treating recombinant precursor protein with mercaptan in alkali
 PT and in presence of chaotropic agent, then isolation on
 PT hydrophobic resin
 XX

PS Disclosure; Page 11; 15pp; German.

CC Pro-insulin is produced by treating recombinant precursor protein
 CC with a mercaptan to provide 2-10 SH residues per Cys residue, in
 CC presence of a chaotropic agent and in aq. medium of pH 10-11,
 CC treating the prod. with 3-50 g hydrophobic adsorber resin per 1 aq.
 CC medium of pH 4-7, isolating the adsorbed resin and pro-insulin and
 CC desorbing the pro-insulin. This method produces pro-insulin with
 CC correctly bonded Cys bridges. Compared with known methods it
 CC involves fewer stages (esp. no sulphitolysis or cyanogen bromide
 CC cleavage) and overall losses during purification are reduced, i.e.
 CC the process is quicker and gives better yields.
 CC Sequences of insulin chain A, B and C are given in AAR68895-97.
 CC Sequences of pro-insulin 1-4 are given in AAR68898-901.

XX Sequence 96 AA;

Query Match 96.2%; Score 152; DB 15; Length 96;
 Best Local Similarity 96.9%; Pred. No. 6.3e-14;
 Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MAPTSSSTKTKTQLEHLLKLQMLINGINNY 32
 DB 1 MAPTSSSTKTKTQLEHLLKLQMLINGINNY 32

RESULT 9

AAR78662
 ID AAR78662 standard; protein; 96 AA.

AC AAR78662;

XX 03-APR-1996 (first entry)

DE Fusion protein contg. proinsulin sequence 3.

XX Proinsulin; post-translational modification; recombinant production;
 KW protein folding; conformation.

XX Synthetic.

XX Key Location/Qualifiers
 FT Region 41..44

FT /label= R2

FT /note= "a peptide of 4 amino acids"

FT Peptide 45..74

FT /label= R1-(B2-B29)-Y

FT /note= "human insulin B-chain"

FT Region 75

FT /label= X

FT Peptide 76..96

FT /label= Gly-(A2-A20)-R3

FT /note= "human insulin A-chain"

XX EP668292-A2.

XX 23-AUG-1995.

XX

PF 09-FEB-1995; 95EP-0101748.
 XX
 PR 18-FEB-1994; 94DE-4405179.
 XX
 PA (FARH) HOECHST AG.
 XX
 PI Gerl M, Ludwig J, Obermeier R, Sabel W;
 XX
 DR WPI; 1995-284754/38.

PT Isolation of insulin that is correctly post-translationally
 PT processed - by reacting pro-insulin with a mercaptan in the presence
 PT of a chaotropic agent and purific. after absorption to hydrophobic
 PT resin
 XX

XX Example 2; Page 8; 16pp; German.

CC The present sequence is that of a fusion protein, produced in E.coli
 CC which contains an example of a proinsulin molecule corresp.
 CC to the general formula R2-R1-(B2-B29)-Y-X-Gly-(A2-A20)-R3 (II). In
 CC formula (II), X = Lys, Arg or a peptide of 2-35 amino acids contg.
 CC Lys or Arg at the N- and C-termini; Y = a natural amino acid; R1 =
 CC Phe or a bond; R2 = H, Arg, Lys, a peptide of 2-45 amino acids
 CC contg. Arg or Lys at the N- and C-termini; R3 = a natural amino
 CC acid; (A2-A20) and (B2-B29) are the insulin A- and B-chain sequences
 CC from human or other insulin. The proinsulin molecule, released by
 CC cyanogen bromide, is reacted with mercaptan at a ratio of 2-10 SH
 CC residues of mercaptan per Cys residue of proinsulin. The reaction
 CC takes place in the presence of a chaotropic auxiliary agent at
 CC pH 10-11 and results in proinsulin with correctly linked cystine
 CC bridges. Reaction with trypsin and opt. carboxypeptidase B yields
 CC correctly folded insulin. The insulin is isolated by absorption on
 CC a hydrophobic resin.

XX Sequence 96 AA;

Query Match 96.2%; Score 152; DB 16; Length 96;
 Best Local Similarity 96.9%; Pred. No. 6.3e-14;
 Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MAPTSSSTKTKTQLEHLLKLQMLINGINNY 32
 DB 1 MAPTSSSTKTKTQLEHLLKLQMLINGINNY 32

RESULT 10

AAR22595

ID AAR22595 standard; Protein; 133 AA.

XX AAR22595;

XX 03-NOV-1992 (first entry)

DE Interleukin-2 used to make hybrid proteins.

XX IL-2; hybrid; diphtheria; toxin; DT; proliferation; peripheral blood;
 KW mononuclear cells; PBMC; auto-immune response; diabetes; rheumatoid;
 KW arthritis; allograft rejection; T-suppressor.

XX Homo sapiens.

XX WO9206117-A.

XX 16-APR-1992.

XX 27-SEP-1991; 91WO-US07342.

XX 28-SEP-1990; 90US-0590113.

XX (SERA-) SERAGEN INC.

XX (UYHO-) UNIVERSITY HOSPITAL.

XX Murphy JR, Svrluga R;

XX WPI; 1992-150820/18.
 DR N-PSDB; AAQ23867.
 XX
 PT Hybrid protein comprising portion of the IL-2 binding domain -
 PT useful for inhibiting unwanted immune responses e.g. autoimmune
 PT diseases and reaction to organ and tissue transplants
 XX
 PS Disclosure; Fig 1; 37pp; English.
 XX
 CC The interleukin-2 protein is part of a hybrid protein comprising
 CC the binding domain of IL-2 and an enzymatically inactive fragment
 CC of diphtheria toxin which does not include a functional DT
 CC generalised eukaryotic binding site (see AAR26486). The hybrid
 CC protein is capable of stimulating the proliferation of peripheral
 CC blood mononuclear cells in vitro and of suppressing an immune
 CC response in a mammal in vivo. The hybrid protein allows the
 CC inhibition of an unwanted immune response such as autoimmune disease,
 CC e.g. diabetes and rheumatoid arthritis, or allograft rejection. It
 CC does not cause general immunosuppression, so avoids the resulting
 CC risk of life threatening infections. In the treatment of allograft
 CC rejection the hybrid protein spares donor-specific T-suppressor cells,
 CC which can thus proliferate and aid in prolonging graft survival. The
 CC hybrid protein does not need to be tailored to individual patients but
 CC can be used as a universal inhibiting agent. Therapy need not be
 CC continuous following allograft or an acute stage of autoimmune
 CC disease, but can be discontinued after a course of treatment.
 XX
 SQ Sequence 133 AA;

Query Match 96.2%; Score 152; DB 13; Length 133;
 Best Local Similarity 96.9%; Pred. No. 9e-14;
 Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MAPTSSSTKKTQLQLEHLLKLQMLNGINNY 32
 |||||
 DB 1 MAPTSSSTKKTQLQLEHLLKLQMLNGINNY 32

RESULT 11

AAP40050
 ID AAP40050 standard; Protein; 134 AA.

AC AAP40050;

DT 14-JAN-1992 (first entry)

DE Sequence of an interleukin-2-like polypeptide encoded by the DNA
 DE insert of pSV-hIL2-O or pSV-hIL2-1.

KW Diagnosis; therapy; cancer; tumour-specific cytotoxic cell; AIDS;
 KW multiple sclerosis; lupus; rheumatoid arthritis; herpes;
 KW viral disease; lymphokine.

XX Homo sapiens.

XX EP118977-A.

XX 19-SEP-1984.

XX 25-JAN-1984; 84EP-0300439.

XX 10-JUN-1983; 83GB-0015981.

XX 08-FEB-1983; 83GB-0003383.

XX (BIOJ) BIOGEN NV.

XX Fliers WC, Devos RR;

XX WPI; 1984-232548/38.

DR N-PSDB; AAN40042.

PT Prodn. of human interleukin 2-like polypeptide(s) - useful

PT instead of IL-2 for stimulating the immune system etc.
 XX
 PS Claim 6; Page 57-58; 69pp; English.

XX The DNA sequence is esp. selected from a human chromosomal gene bank,
 CC e.g. it is a hIL-2 related portion of lamda CH4A-ghIL-2-1 or -2, or
 CC of lamda I47-ghIL-2-1, -2 or -3. Transformed hosts are also claimed,
 CC esp. E.coli, Ps spp., B.subtilis, B.stearothermophilus. IL-2-like
 CC polypeptides are also claimed.

XX Sequence 134 AA;

Query Match 96.2%; Score 152; DB 5; Length 134;
 Best Local Similarity 96.9%; Pred. No. 9.1e-14;
 Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MAPTSSSTKKTQLQLEHLLKLQMLNGINNY 32
 |||||
 DB 1 MAPTSSSTKKTQLQLEHLLKLQMLNGINNY 32

RESULT 12

AAP50053

ID AAP50053 standard; Protein; 134 AA.

AC AAP50053;

DT 16-AUG-2002 (updated)

DT 03-SEP-1991 (first entry)

XX Sequence 1 of new biologically active interleukin 2 (IL-2).

XX Immunological agent; lymphokine.

XX Homo sapiens.

XX Synthetic.

XX EP163249-A.

XX 04-DEC-1985.

XX 28-MAY-1985; 85EP-0113324.

XX 29-MAY-1984; 84DE-3419995.

XX (FARH) HOECHST AG.

XX Engels J, Uhlmann E, Wengenmayer F, Mullner H, Winnacker EL;
 PI Mertz R, Okazaki H;

XX WPI; 1985-304738/49.

XX N-PSDB; AAN50037.

XX New biologically active interleukin 2 fragments and derivs. - and
 PT coding DNA sequences, intermediate oligo-nucleotide(s), hybrid
 PT plasmid(s) and transformed cells

XX Disclosure; Page 18-20; 33pp; German.

XX DNA SQs coding for AAs 1-133 and 0-133 (an additional Met) of IL-2
 CC are claimed, including the CDS of SQ I (see AAN50037) without 1
 CC or 2 stop codons. The use of a synthetic gene is esp. convenient
 CC for expression in E. coli and allows modification of the AA SQ to
 CC improve peptide stability, solubility or activity. The synthetic
 CC gene was made from a series of oligonucleotides ligated to form four
 CC larger fragments designated If 2-I to 2-IV (see AAN50038).
 CC (Updated on 16-AUG-2002 to add missing OS field.)

XX Sequence 134 AA;

Query Match 96.2%; Score 152; DB 6; Length 134;

Best Local Similarity 96.9%; Pred. No. 9.1e-14;

Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAPSSSTKKTKQLQLEHLLKLQMLINGINNY 32
 DB 1 MAPSSSTKKTKQLQLEHLLKLQMLINGINNY 32

RESULT 13

AAP50855
 ID AAP50855 standard; Protein; 134 AA.

XX AC AAP50855;
 XX DT 03-OCT-2002 (updated)
 DT 01-DEC-1991 (first entry)
 XX XX

DE Sequence encoded by synthetic interleukin II (IL-2) gene.

KW Immunotherapy; lymphokine; interleukin-2; thymocyte mitogenesis.

OS Synthetic.

PN WO8500817-A.

PD 28-FEB-1985.

XX PF 09-AUG-1984; 84WO-US01252.

PR 03-AUG-1984; 84US-0635941.

PR 10-AUG-1983; 83US-0521967.

XX PA (AMGE-) AMGEN.

XX PI Souza LM, Stabinsky Y;

DR WPI; 1985-062280/10.

DR N-PSDB; AAN50535.

XX Microbial expression of interleukin II and analogues - by using
 PT manufactured DNA sequences to transform microorganisms

XX Example; Table IV, Page 15-16; 39pp; English.

XX The inventors claim a manufactured gene for the prodn. of IL-2 and
 CC analogues, and for polypeptides of IL-2 and analogues, and for
 CC methods for their recombinant production.
 CC (Updated on 03-OCT-2002 to add missing OS field.)

XX Sequence 134 AA;

Query Match 96.2%; Score 152; DB 6; Length 134;
 Best Local Similarity 96.9%; Pred. No. 9.1e-14;
 Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAPSSSTKKTKQLQLEHLLKLQMLINGINNY 32
 DB 1 MAPSSSTKKTKQLQLEHLLKLQMLINGINNY 32

RESULT 14

AAP61102
 ID AAP61102 standard; Protein; 134 AA.

XX AC AAP61102;

XX DT 09-MAR-1992 (first entry)

DE Sequence of mature human interleukin 2 (IL2) encoded by SUN-IL2.

XX KW Yeast expression vector; lymphokine.

XX OS Homo sapiens.

XX PN EP171000-A.

XX PD 12-FEB-1986.
 XX XX
 XX PF 26-JUL-1985; 85EP-0109405.
 XX XX
 XX PR 27-JUL-1984; 84JP-0157038.
 XX XX
 XX PA (SUNR) SUNTORY LTD.
 XX XX
 XX PI Oshima T, Tanaka S, Tsujimoto M, Nakazato H;
 XX XX
 XX DR WPI; 1986-043554/07.
 DR N-PSDB; AAN60198.
 XX XX
 PT Protein and peptide prodn. by immobilised yeast transformant -
 PT contg. expression vector which induces secretion of prod. from
 PT cell into culture medium
 XX XX
 PS Disclosure; Fig 6 and Page 31; 53pp; English.

XX CC The inventors claim a method for the prodn. of a substance having
 CC the AA SQ of AAP61102. The method uses a synthetic DNA SQ (AAN60198). A
 CC composition contg. a protein having human IL2 activity which is
 CC produced by the method is also claimed. The method uses yeast
 CC transformed by a secretory expression vector.
 XX XX

SQ Sequence 134 AA;

Query Match 96.2%; Score 152; DB 7; Length 134;
 Best Local Similarity 96.9%; Pred. No. 9.1e-14;
 Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAPSSSTKKTKQLQLEHLLKLQMLINGINNY 32
 DB 1 MAPSSSTKKTKQLQLEHLLKLQMLINGINNY 32

RESULT 15

AAP70585
 ID AAP70585 standard; protein; 134 AA.

XX AC AAP70585;

XX DT 10-APR-1991 (first entry)

XX DE Sequence of human interleukin-2 (IL-2).

XX KW Lymphokine.

XX OS Homo sapiens.

XX PN DE3541856-A.

XX PD 04-JUN-1987.

XX PF 27-NOV-1985; 85DE-3541856.

XX PR 27-NOV-1985; 85DE-3541856.

XX PA (FARH) HOECHST AG.

XX PI Habermann P, Wengenmayer F;

XX DR WPI; 1987-157830/23.

XX DR N-PSDB; AAN70931.

XX Fusion proteins contg. interleukin 2 aminoacid sequences - as
 PT well as genes coding for these proteins, vectors contg. the
 PT genes, and host cells contg. the vectors
 XX Example; pp 7-8; 20pp; German.

XX Prefd. fusion proteins are of formula Met-X-Y-Z or Met-2-Y-X. Where

CC X-an AA sequence corresp. essentially to approx. the first 100 AAs
CC of human interleukin-2; Y-a direct bond or bridge of genetically
CC codable AAs which facilitates the cleaving off of the AA sequence Z;
CC Z-a sequence of genetically codable AAs.

XX

SQ Sequence 134 AA;

Query Match 96.2%; Score 152; DB 8; Length 134;
Best Local Similarity 96.9%; Pred. No. 9.1e-14;
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAPTSSSTKKTQLEHLLKLMILGINNY 32

|||||
Db 1 MAPTSSSTKKTQLEHLLKLMILGINNY 32

Search completed: February 20, 2003, 10:05:03
Job time : 31.9841 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 20, 2003, 10:03:27 ; Search time 28.9524 Seconds
(without alignments)
106.254 Million cell updates/sec

Title: US-09-776-781-6
Perfect score: 158
Sequence: 1 MAPTSSSTKKTQLEHLLKLQMLNGINNY 32

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR73:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB ID	Description
1	147	93.0	153	1	ICHU2
2	147	93.0	153	1	ICG12
3	107	67.7	154	2	JN0698
4	97	61.4	155	2	A31278
5	96	60.8	154	2	S16241
6	95	60.1	155	2	S33509
7	85	53.8	149	2	S31391
8	72	45.6	155	2	S38662
9	72	45.6	155	2	S11488
10	72	45.6	155	2	I45913
11	69	43.7	169	2	S37289
12	64	40.5	169	1	ICMS2
13	61	38.6	189	2	H64307
14	54	34.2	1061	1	GNLJG4
15	53	33.5	357	2	S12169
16	53	33.5	452	2	B84483
17	52.5	32.6	60	2	I68870
18	51.5	32.6	62	2	I84512
19	51.5	32.6	415	2	I31637
20	51	32.3	737	2	G82262
21	51	32.3	866	2	F64625
22	51	32.3	875	2	B71890
23	50.5	32.0	72	2	I68871
24	50.5	32.0	741	2	A45771
25	50	31.6	304	2	F95285
26	50	31.6	543	2	F82217
27	49.5	31.3	367	2	E84453
28	49.5	31.3	474	2	S31712
29	49	31.0	145	2	H83921

30	48.5	30.7	288	2	B89930
31	48.5	30.7	452	2	G84679
32	48	30.4	398	2	B70209
33	48	30.4	441	2	AB1367
34	48	30.4	441	2	AC1736
35	48	30.4	765	2	S76795
36	48	30.4	1964	2	A59282
37	47.5	30.1	127	1	NR0K2
38	47.5	30.1	244	2	T11685
39	47	29.7	257	2	S39521
40	47	29.7	307	2	T46103
41	47	29.7	406	2	S24788
42	47	29.7	432	2	S08277
43	47	29.7	511	2	D71687
44	47	29.7	531	2	T33319
45	47	29.7	564	2	S76672

ALIGNMENTS

RESULT 1

ICHU2
N:Interleukin-2 precursor [validated] - human
N:Alternate names: IL-2; T-cell growth factor
C:Species: Homo sapiens (man)
C:Date: 11-Aug-1983 #sequence_revision 11-Aug-1983 #text_change 08-Dec-2000
C:Accession: A01849; A21192; A20961; S31209; A93297; A90113; A93478; I56518; I73624;
R:Holbrook, N.J.; Lieber, M.; Crabtree, G.R.
Nucleic Acids Res. 12, 5005-5013, 1984
A:Title: DNA sequence of the 5' flanking region of the human interleukin 2 gene: homo
A:Reference number: A93524; MUID:84247353; PMID:6330695
A:Accession: A01849
A:Molecule type: DNA
A:Residues: 1-153 <HO2>
A:Cross-references: GB:X00695; GB:X00200; GB:X00201; GB:X00202; NID:g33783; PIDN:CAA2
R:Fujita, T.; Takooka, C.; Matsui, H.; Taniguchi, T.
Proc. Natl. Acad. Sci. U.S.A. 80, 7437-7441, 1983
A:Title: Structure of the human interleukin 2 gene.
A:Reference number: A21192; MUID:84170243; PMID:6324170
A:Accession: A21192
A:Molecule type: DNA
A:Residues: 1-153 <FU>
A:Cross-references: GB:J00264; NID:gl86294; PIDN:AAD48509.1; PID:g579676
R:Holbrook, N.J.; Smith, K.A.; Fornace Jr., A.J.; Comeau, C.M.; Wiskocil, R.L.; Crabt
Proc. Natl. Acad. Sci. U.S.A. 81, 1634-1638, 1984
A:Title: T-cell growth factor: complete nucleotide sequence and organization of the g
A:Reference number: A20961; MUID:84170356; PMID:6608729
A:Accession: A20961
A:Molecule type: DNA
A:Residues: 1-153 <HO2>
A:Cross-references: GB:K02056; NID:gl86302; PIDN:AAA98792.1; PID:g386819
R:Laabi, Y.; Gras, M.P.; Carbonnel, F.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Tsapi
EMBO J. 11, 3897-3904, 1992
A:Title: A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene by a t(
A:Reference number: S31208; MUID:93010984; PMID:1396583
A:Accession: S31209
A:Molecule type: mRNA
A:Residues: 11-117 <LAA>
A:Cross-references: EMBL:Z14955
A:Note: this sequence is shown from the beginning of the fragment to the chromosomal
R:Taniguchi, T.; Matsui, H.; Fujita, T.; Takooka, C.; Kashima, N.; Yoshimoto, R.; Ham
Nature 302, 305-310, 1983
A:Title: Structure and expression of a cloned cDNA for human interleukin-2.
A:Reference number: A93297; MUID:83167472; PMID:6403867
A:Accession: A93297
A:Molecule type: mRNA
A:Residues: 1-153 <TAN>
A:Cross-references: GB:V00564; NID:g33780; PIDN:CAA23827.1; PID:g33781
A:Experimental source: leukemic T-cell line, Jurkat-111, cloned from Jurkat-FHCRC
R:Maeda, S.; Nishino, N.; Obaru, K.; Mita, S.; Nomiya, H.; Shimada, K.; Fujimoto, K
Biochem. Biophys. Res. Commun. 115, 1040-1047, 1983
A:Title: Cloning of interleukin 2 mRNAs from human tonsils.

A:Reference number: A90113; MUID:84023840; PMID:6312994
A:Accession: A90113
A:Molecule type: mRNA
A:Residues: 1-153 <MAE>
A:Cross-references: GB:J00264; NID:g186294; PIDN:AA48509.1; PID:g5729676
A:Experimental source: tonsillar mononuclear cells
R:DeVos, R.; Platinck, G.; Cheroutre, H.; Simons, G.; Degraeve, W.; Tavernier, J.; Remau
Nucleic Acids Res. 11, 4307-4323, 1983
A:Title: Molecular cloning of human interleukin 2 cDNA and its expression in Escherichia
A:Reference number: A93478; MUID:83246551; PMID:6306584
A:Accession: A93478
A:Molecule type: mRNA
A:Residues: 1-153 <DEV>
A:Cross-references: GB:V00564; NID:g33780; PIDN:CAA23827.1; PID:g33781
A:Experimental source: splenocytes
R:Elzenberg, O.; Faber-Elman, A.; Lotan, M.; Schwartz, M.
J. Neurochem. 64, 1928-1936, 1995
A:Title: Interleukin-2 transcripts in human and rodent brains: possible expression by as
A:Reference number: I56518; MUID:95239150; PMID:7722480
A:Accession: I56518
A:Molecule type: mRNA
A:Status: translated from GB/EMBL/DBJ
A:Residues: 1-152 <EIZ>
A:Cross-references: GB:S77834; NID:g999000
A:Accession: I73624
A:Molecule type: mRNA
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Residues: 5-7,'F','9-17','P','19-32','X','34-45','X','47-143 <RES>
A:Cross-references: GB:S77835; NID:g999001; PIDN:AA414264.1; PID:g4261964
R:Nishino, N.; Obaru, K.; Maeda, S.; Shimada, K.; Onoue, K.
Biomed. Res. 6, 197-205, 1985
A:Title: Organization of the DNA regions flanking the human interleukin 2 gene.
A:Reference number: I52528
A:Accession: I52528
A:Molecule type: DNA
A:Status: translated from GB/EMBL/DBJ
A:Residues: 1-68 <RE2>
A:Cross-references: GB:M33199; NID:g186296; PIDN:AAA59139.1; PID:g553508
R:Sleibnlist, U.; Durand, D.B.; Bressler, P.; Holbrook, N.J.; Norris, C.A.; Kamoun, M.;
Mol. Cell. Biol. 6, 3042-3049, 1986
A:Title: Promoter region of interleukin-2 gene undergoes chromatin structure changes and
A:Reference number: I57603; MUID:87064618; PMID:3491296
A:Accession: I57603
A:Molecule type: DNA
A:Status: translated from GB/EMBL/DBJ
A:Residues: 1-68 <RE3>
A:Cross-references: GB:M13879; NID:g186305; PIDN:AAA59141.1; PID:g553509
R>Weir, M.P.; Chaplin, M.A.; Wallace, D.M.; Dykes, C.W.; Hobden, A.N.
Biochemistry 27, 6883-6892, 1988
A:Title: Structure-activity relationships of recombinant human interleukin 2.
A:Reference number: I52401; MUID:89062420; PMID:3264184
A:Contents: recombinant IL-2 and mutants expressed in E. coli
A:Accession: I52401
A:Molecule type: DNA
A:Status: translated from GB/EMBL/DBJ
A:Residues: 'M', 21-153 <RE4>
A:Cross-references: GB:M22005; NID:g186300; PIDN:AAA59140.1; PID:g386818
A:Note: mutation of Phe-42 to Ala reduced binding to the IL-2 receptor 5-10 fold without
R:Robb, R.J.; Kutny, R.M.; Panico, M.; Morris, H.R.; Chowdhry, V.
Proc. Natl. Acad. Sci. U.S.A. 81, 6486-6490, 1984
A:Title: Amino acid sequence and post-translational modification of human interleukin 2.
A:Reference number: A94009; MUID:85038540; PMID:6333684
A:Accession: A94009
A:Molecule type: protein
A:Residues: 21-153 <ROB>
A:Note: disulfide bonds and carbohydrate binding site were determined
A:Note: heterogeneity in Jurkat-derived IL-2 is primarily due to differences in glycosyl
n in lacking 21-Ala (FT-IL2-A and FT-IL2-B) and 22-Pro (FT-IL2-B)
R:Conradt, H.S.; Nimtz, M.; Dittmar, K.E.J.; Lindenmaier, W.; Hoppe, J.; Hauser, H.
J. Biol. Chem. 264, 17368-17373, 1989
A:Title: Expression of human interleukin-2 in recombinant baby hamster kidney, Ltk-, and
de.
A:Reference number: A34463; MUID:90008901; PMID:2793860

A:Accession: A34463
A:Molecule type: protein
A:Residues: 21-35 <CON>
A:Note: the O-linked glycosylation site in recombinant material matched that from hum
R:Grabenhorst, E.; Hofer, B.; Nimtz, M.; Jaeger, V.; Conradt, H.S.
Eur. J. Biochem. 215, 189-197, 1993
A:Title: Biosynthesis and secretion of human interleukin 2 glycoproteins variants fro
A:Reference number: S34052; MUID:93345493; PMID:8344280
A:Contents: annotation; glycosylation of variant forms expressed in insect cells
A:Genetics:
A:Gene: GDB:IL2
A:Cross-references: GDB:IL9344; OMIM:147680
A:Map position: 4q26-4q27
A:Introns: 49/3; 69/3; 117/3
C:Superfamily: Interleukin-2
C:Keywords: cytokine; glycoprotein; growth factor; immunoregulation; lymphokine; T-ce
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-153/Product: interleukin-2 #status experimental <IL2>
F;23/Binding site: carbohydrate (Thr) (covalent) #status experimental
F;78-125/Disulfide bonds: #status experimental
Query Match 93.0%; Score 147; DB 1; Length 153;
Best Local Similarity 96.8%; Pred. No. 7.4e-14;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 APTSSSTKTKTQLQLEHLLKLQMLINGINNY 32
|||||
Db 21 APTSSSTKTKTQLQLEHLLKLQMLINGINNY 51
|||||
RESULT 2
ICG12
Interleukin-2 precursor - common gibbon
N:Alternate names: IL-2; T-cell growth factor
C:Species: Hylobates lar (common gibbon, white-handed gibbon)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 22-Jun-1999
C:Accession: A94067; A01849
R:Chen, S.J.; Holbrook, N.J.; Mitchell, K.F.; Vallone, C.A.; Greengard, J.S.; Crabtre
Proc. Natl. Acad. Sci. U.S.A. 82, 7284-7288, 1985
A:Title: A viral long terminal repeat in the interleukin 2 gene of a cell line that c
A:Reference number: A94067; MUID:86042650; PMID:3877307
A:Accession: A94067
A:Molecule type: mRNA
A:Residues: 1-153 <CHE>
A:Cross-references: GB:M11144; NID:g177014; PIDN:AAA35454.1; PID:g177015
A:Experimental source: leukemia cell line M1A 144; ATCC TIB 201
A:Note: the integration of a retrovirus sequence containing a 5' LTR into the 3' nonc
C:Superfamily: Interleukin-2
C:Keywords: cytokine; glycoprotein; growth factor; immunoregulation; lymphokine; T-ce
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-153/Product: interleukin-2 #status predicted <IL2>
F;23/Binding site: carbohydrate (Thr) (covalent) #status predicted
F;78-125/Disulfide bonds: #status predicted
Query Match 93.0%; Score 147; DB 1; Length 153;
Best Local Similarity 96.8%; Pred. No. 7.4e-14;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 APTSSSTKTKTQLQLEHLLKLQMLINGINNY 32
|||||
Db 21 APTSSSTKTKTQLQLEHLLKLQMLINGINNY 51
|||||
RESULT 3
JN0698
Interleukin 2 precursor - cat
C:Species: Felis silvestris catus (domestic cat)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 16-Jul-1999
C:Accession: JN0698
R:Cozzi, P.J.; Padrid, P.A.; Takeda, J.; Alegre, M.L.; Yuhki, N.; Leff, A.R.
Biochem. Biophys. Res. Commun. 194, 1038-1043, 1993
A:Title: Sequence and functional characterization of feline interleukin 2.
A:Reference number: JN0698; MUID:93356765; PMID:8352761

```
A:Accession: JN0698
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-154 <COZ>
A:Cross-references: GB:L19402; NID:g304313; PIDN:AAA02865.1; PID:g304314
C:Superfamily: interleukin-2
C:Keywords: growth factor

Query Match      67.7%; Score 107; DB 2; Length 154;
Best Local Similarity 70.0%; Pred. No. 4.5e-08;
Matches 21; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY  2 APTSSSTKKTQQLQLEHLLKLQMLINGINN 31
Db   21 APASSTKETQQLQLEHLLKLQMLINGVNN 50

RESULT 4
A31278
interleukin-2 precursor - rat
N:Alternate names: IL-2; T-cell growth factor
C:Species: Rattus norvegicus (Norway rat)
C:Date: 26-Apr-1989 #sequence_revision 26-Apr-1989 #text_change 16-Jul-1999
C:Accession: A45882; A31278
R:McKnight, A.J.; Mason, D.W.; Barclay, A.N.
Immunogenetics 30, 145-147, 1989
A:Title: Sequence of rat interleukin 2 and anomalous binding of a mouse interleukin 2 c
A:Reference number: A45882; MUID:89339608; PMID:2788130
A:Accession: A45882
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-155 <MCK>
A:Cross-references: GB:M22899; NID:g204909; PIDN:AAA41427.1; PID:g204910
C:Superfamily: interleukin-2
C:Keywords: cytokine; glycoprotein; growth factor; immunoregulation; T-cell

Query Match      61.4%; Score 97; DB 2; Length 155;
Best Local Similarity 64.5%; Pred. No. 1.3e-06;
Matches 20; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY  2 APTSSSTKKTQQLQLEHLLKLQMLINGINN 32
Db   21 APTSSPAKETQQLQLEHLLKLQMLINGIDNY 51

RESULT 5
S16241
interleukin-2 precursor - pig
N:Alternate names: IL-2; T-cell growth factor
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 16-Jul-1999
C:Accession: S16241; S15473
R:Goodall, J.C.; Emery, D.C.; Bailey, M.; English, L.S.; Hall, L.
Biochim. Biophys. Acta 1089, 257-258, 1991
A:Title: cDNA cloning of porcine interleukin 2 by polymerase chain reaction.
A:Reference number: S16241; MUID:91274360; PMID:2054386
A:Accession: S16241
A:Molecule type: mRNA
A:Residues: 1-154 <GOO>
A:Cross-references: EMBL:X56750; NID:g1991; PIDN:CAA40071.1; PID:g1992
R:Lefevre, F.
submitted to the EMBL Data Library, March 1991
A:Description: Molecular cloning of porcine interleukin 2 cDNA by the polymerase chain r
A:Reference number: S15473
A:Accession: S15473
A:Molecule type: mRNA
A:Residues: 1-154 <LEF>
A:Cross-references: EMBL:X58428; NID:g2068; PIDN:CAA41330.1; PID:g2069
C:Superfamily: interleukin-2
C:Keywords: cytokine; glycoprotein; growth factor; immunoregulation; T-cell
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-154/Product: interleukin-2 #status predicted <MAT>

Query Match      60.8%; Score 96; DB 2; Length 154;
Best Local Similarity 64.5%; Pred. No. 1.7e-06;
Matches 20; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY  2 APTSSSTKKTQQLQLEHLLKLQMLINGINN 32
Db   21 APTSSSTANTKQLEPLLDLQLLKEVKNY 51

RESULT 6
S33509
interleukin-2 - Mongolian jird
C:Species: Meriones unguiculatus (Mongolian jird)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Jul-1999
C:Accession: S33509
R:Ma, Z.; Klei, T.; Horohov, D.
submitted to the EMBL Data Library, October 1992
A:Description: Cross-species PCR cloning of Jird (Meriones unguiculatus) interleukin-
A:Reference number: S33509
A:Accession: S33509
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-155 <MAI>
A:Cross-references: EMBL:X68779; NID:g577588; PIDN:CAA48679.1; PID:g311638
C:Superfamily: interleukin-2

Query Match      60.1%; Score 95; DB 2; Length 155;
Best Local Similarity 64.5%; Pred. No. 2.5e-06;
Matches 20; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

QY  2 APTSSSTKKTQQLQLEHLLKLQMLINGINN 32
Db   21 APTSSPAKEAQQLQLEHLLKLQMLINGINNY 51

RESULT 7
S31391
interleukin-2 precursor - horse
C:Species: Equus caballus (domestic horse)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
C:Accession: S31391
R:Tavernor, A.S.; Butcher, G.W.
submitted to the EMBL Data Library, November 1992
A:Description: cDNA cloning of equine interleukin-2 by polymerase chain reaction.
A:Reference number: S31391
A:Accession: S31391
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-149 <TAV>
A:Cross-references: EMBL:X69393; NID:g1076; PIDN:CAA49190.1; PID:g1077
C:Superfamily: interleukin-2

Query Match      53.8%; Score 85; DB 2; Length 149;
Best Local Similarity 53.3%; Pred. No. 6.5e-05;
Matches 16; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY  2 APTSSSTKKTQQLQLEHLLKLQMLINGINN 31
Db   21 APTSSSKRETQQLQLEHLLKLQMLINGVNN 50

RESULT 8
S38662
interleukin-2 - goat
C:Species: Capra aegagrus hircus (domestic goat)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Jul-1999
C:Accession: S38662
R:Rimstad, E.
submitted to the EMBL Data Library, November 1993
A:Description: The molecular cloning and expression of caprine interleukin 2.
A:Reference number: S38662
A:Accession: S38662
A>Status: preliminary
```

A:Molecule type: mRNA
A:Residues: 1-155 <RIM>
A:Cross-references: EMBL:X76063; NID:g416002; PIDN:CAA53664.1; PID:g416003
C:Superfamily: Interleukin-2

Query Match 45.6%; Score 72; DB 2; Length 155;
Best Local Similarity 50.0%; Pred. No. 0.0052;
Matches 15; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLOLEHLLKLQMLNGINN 31
||||||| | : : : ||| | : |
Db 21 APTSSSTGMTKMKVSKLLDLQLLEKVN 50

RESULT 9

S11488

Interleukin-2 precursor - sheep

C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999

C:Accession: S11488; S13102; S15517

R:Goodall, J.C.; Emery, D.C.; Perry, A.C.F.; English, L.S.; Hall, L.

Nucleic Acids Res. 18, 5883, 1990

A:Title: cDNA cloning of ovine interleukin 2 by PCR.

A:Reference number: S11488; MUID:91016933; PMID:2216781

A:Accession: S11488

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-155 <GOO>

A:Cross-references: EMBL:X53934; NID:g1281; PIDN:CAA37881.1; PID:g1282

R:Scow, H.F.; Rothel, J.S.; Radford, A.J.; Wood, P.R.

Nucleic Acids Res. 18, 7175, 1990

A:Title: The molecular cloning of ovine interleukin 2 gene by the polymerase chain react

A:Reference number: S13102; MUID:91088336; PMID:2263496

A:Accession: S13102

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-5, 'L', 7-155 <SEO>

A:Cross-references: EMBL:X55641; NID:g1810; PIDN:CAA39165.1; PID:g1811

R:Bujdosó, R.; Williamson, M.L.; Sargan, D.R.; Hein, W.H.; McConnell, I.

submitted to the EMBL Data Library, April 1991

A:Reference number: S15517

A:Accession: S15517

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 21-153 <BUJ>

A:Cross-references: EMBL:X60148

C:Superfamily: Interleukin-2

Query Match 45.6%; Score 72; DB 2; Length 155;
Best Local Similarity 50.0%; Pred. No. 0.0052;
Matches 15; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLOLEHLLKLQMLNGINN 31
||||||| | : : : ||| | : |
Db 21 APTSSSTGMTKMKVSKLLDLQLLEKVN 50

RESULT 10

I45913

Interleukin-2 precursor - bovine

C:Species: Bos primigenius taurus (cattle)

C:Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 16-Jul-1999

C:Accession: I45913; S21470; S20761

R:Cerretti, D.P.; McKerghan, K.; Larsen, A.; Cantrell, M.A.; Anderson, D.; Gillis, S.;

Proc. Natl. Acad. Sci. U.S.A. 83, 3223-3227, 1986

A:Title: Cloning, sequence, and expression of bovine interleukin 2.

A:Reference number: I45913; MUID:86205869; PMID:3517854

A:Accession: I45913

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-155 <CER>

A:Cross-references: GB:M12791; NID:g163204; PIDN:AAA30586.1; PID:g163205

R:Anikeeva, N.N.; Vinogradova, T.V.; Votoshin, O.N.

submitted to the EMBL Data Library, December 1989
A:Reference number: S21470

A:Accession: S21470

A:Molecule type: DNA

A:Residues: 1-22 <AN2>

A:Cross-references: EMBL:X17201; NID:g452; PIDN:CAA35062.1; PID:g453

C:Genetics:

A:Gene: IL-2

C:Superfamily: Interleukin-2

C:Keywords: cytokine; glycoprotein; growth factor; immunoregulation; lymphokine; T-ce

Query Match 45.6%; Score 72; DB 2; Length 155;
Best Local Similarity 50.0%; Pred. No. 0.0052;
Matches 15; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLOLEHLLKLQMLNGINN 31
||||||| | : : : ||| | : |
Db 21 APTSSSTGMTKMKVSKLLDLQLLEKVN 50

RESULT 11

S37289

Interleukin-2 precursor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999

C:Accession: S37289; S27205; S36162; S24936

R:Todd, J.A.

submitted to the EMBL Data Library, April 1993

A:Reference number: S37289

A:Accession: S37289

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-169 <TOD>

A:Cross-references: EMBL:X73040

R:Matesanz, F.; Alcina, A.; Pellicer, A.

Biochim. Biophys. Acta 1132, 335-336, 1992

A:Title: A new cDNA sequence for the murine interleukin-2 gene.

A:Reference number: S27205; MUID:93041941; PMID:1420317

A:Accession: S27205

A:Molecule type: mRNA

A:Residues: 1-63 <MATE>

A:Cross-references: EMBL:X66058; NID:g52725; PIDN:CAA46854.1; PID:g52726

R:Ghosh, S.; Palmer, S.M.; Rodrigues, N.R.; Cordell, H.J.; Hearne, C.M.; Cornall, R.J

Nature Genet. 4, 404-409, 1993

A:Title: Polygenic control of autoimmune diabetes in nonobese diabetic mice.

A:Reference number: S36162; MUID:94004970; PMID:8401590

A:Accession: S36162

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-50 <GHO>

A:Cross-references: EMBL:X73040

C:Superfamily: Interleukin-2

C:Keywords: cytokine; glycoprotein; growth factor; lymphokine; T-cell

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-63/Product: Interleukin-2 #status predicted <MAT>

Query Match 43.7%; Score 69; DB 2; Length 169;
Best Local Similarity 45.9%; Pred. No. 0.015;
Matches 17; Conservative 6; Mismatches 8; Indels 6; Gaps 1;

QY 2 APTSSSTKKTQLO-----LEHLLKLQMLNGINN 32
:||||||| | : : : ||| | : |
Db 29 SPTSSSTAEEAQQQQQQHLEQLLMDLQELLSRMENY 65

RESULT 12

ICMS2

Interleukin-2 precursor - mouse

N:Alternate names: IL-2; T-cell growth factor (TCGF)

C:Species: Mus musculus (house mouse)

C:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 21-Jul-2000

C:Accession: A93550; A54490; I48597; A01850; I84713

R:Fuse, A.; Fujita, T.; Yasumitsu, H.; Kashima, N.; Hasegawa, K.; Taniguchi, T.

Nucleic Acids Res. 12, 9323-9331, 1984

A;Title: Organization and structure of the mouse interleukin-2 gene.
A;Reference number: A93550; MUID:85087940; PMID:6240025
A;Accession: A93550
A;Molecule type: DNA
A;Residues: 1-169 <FUS>
R;Degrave, W.; Simons, G.; Devos, R.; Plaetinck, G.; Remaut, E.; Tavernier, J.; Fiers, W.
Mol. Biol. Rep. 11, 57-61, 1986
A;Title: Cloning and structure of a mouse interleukin-2 chromosomal gene.
A;Reference number: A54490; MUID:86118396; PMID:3003564
A;Accession: A54490
A;Molecule type: DNA
A;Residues: 1-169 <DEG>
A;Cross-references: GB:M16760
R;Yokota, T.; Arai, N.; Lee, F.; Rennick, D.; Mosmann, T.; Arai, K.
Proc. Natl. Acad. Sci. U.S.A. 82, 68-72, 1985
A;Title: Use of a cDNA expression vector for isolation of mouse interleukin 2 cDNA clones
A;Reference number: A94064; MUID:85113172; PMID:3918306
A;Accession: A94064
A;Molecule type: mRNA
A;Residues: 1-169 <YOK>
A;Cross-references: PIDN:AAA39289.1; PID:g309404
R;Kashima, N.; Nishi-Takaoka, C.; Fujita, T.; Taki, S.; Yamada, G.; Hamuro, J.; Taniguchi,
Nature 313, 402-404, 1985
A;Title: Unique structure of murine interleukin-2 as deduced from cloned cDNAs.
A;Reference number: I48597; MUID:85111148; PMID:2578624
A;Accession: I48597
A;Status: preliminary; translated from GB/EMBL/DDBB
A;Molecule type: mRNA
A;Residues: 1-169 <RES>
A;Cross-references: EMBL:X01772; GB:X02797; NID:g52663; PIDN:CAA25909.1; PID:g758159
C;Comment: Produced by T-cells in response to antigenic or mitogenic stimulation, this P
C;Genetics:
A;Introns: 63/3; 83/3; 132/3
C;Superfamily: Interleukin-2
C;Keywords: cytokine; glycoprotein; growth factor; immunoregulation; lymphokine; T-cell
F;1-20/DNA: signal sequence #status predicted <SIG>
F;21-169/Product: interleukin-2 #status predicted <MAT>
F;23/Binding site: carbohydurate (Thr) (covalent) #status predicted
F;92-140/Disulfide bonds: #status predicted

Query Match 40.5%; Score 64; DB 1; Length 169;
Best Local Similarity 37.8%; Pred. No. 0.081;
Matches 17; Conservative 6; Mismatches 8; Indels 14; Gaps 1;

OY 2 APTSSST-----KKTQLQLEHLLKLQMLANGINNY 32
||||||| : || ||: ||: ||: ||
Db 21 APTSSSTSSSTAQAQQQQQQQQQQQHLELLMDLQELLSRMENY 65

RESULT 13
H64307
hypothetical protein MJ0064 - Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C;Accession: H64307
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
rson, J.D.; Sadov, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A;Authors: Kalne, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.
A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A;Reference number: A64300; MUID:96337999; PMID:8688087
A;Accession: H64307
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-189 <SUL>
A;Cross-references: GB:U67464; GB:L77117; NID:g1590852; PIDN:AAB98051.1; PID:g1590855;
C;Genetics:
A;Map position: FOR61888-62457
A;Start codon: GTG

Query Match 38.6%; Score 61; DB 2; Length 189;

C:Genetics:
A;Introns: 12/3; 71/1; 121/3
C:Keywords: acyltransferase
Query Match 33.5%; Score 53; DB 2; Length 357;
Best Local Similarity 52.6%; Pred. No. 7.2;
Matches 10; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
QY 8 TTKTQLQLEHLLKQWIL 26
|||||:|||||:|:|:
Db 40 TTKTQAELEQLLEQVM 58

Search completed: February 20, 2003, 10:07:24
Job time : 30.9524 secs

GenCore version 5.1.1.3
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OM protein - protein search, using sw model

Run on: February 20, 2003, 10:01:02 ; Search time 7.11111 Seconds
(without alignments)
186.643 Million cell updates/sec

Title: US-09-776-781-6

Perfect score: 158

Sequence: 1 MAPSSSTKTKTQLQLEHLLKLQMLNGINNY 32

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Length	DB ID	Description
1	147	93.0	153	1 IL2 HUMAN	P01585 homo sapien
2	147	93.0	154	1 IL2 MACFA	Q29615 macaca fasc
3	147	93.0	154	1 IL2 MACMU	P51498 macaca muba
4	142	89.9	154	1 IL2 CERTO	P46649 cercopithec
5	116	73.4	154	1 IL2 MIRAN	O62641 mirounga an
6	107.5	68.0	155	1 IL2 CANFA	Q29416 canis famil
7	107	67.7	153	1 IL2 RABIT	Q77620 oryctolagus
8	107	67.7	154	1 IL2 FELCA	Q07885 felis silve
9	97	61.4	155	1 IL2 RAT	P17108 rattus norv
10	96	60.8	154	1 IL2 PIG	P26891 sus scrofa
11	95	60.1	155	1 IL2 MERUN	Q08081 meriones un
12	88	55.7	152	1 IL2 ORCOR	O97513 orclinus orc
13	85	53.8	149	1 IL2 HORSE	P37997 equus cabal
14	72	45.6	155	1 IL2 BOVIN	P05016 bos taurus
15	72	45.6	155	1 IL2 CAPHI	P36835 capra hircu
16	72	45.6	155	1 IL2 SHEEP	P19114 ovis aries
17	72	45.6	162	1 IL2 CEREL	P51747 cervus elap
18	64.5	40.8	166	1 IL2 MUSSP	Q08867 mus spretus
19	64	40.5	169	1 IL2 MOUSE	P04351 mus musculu
20	61	38.6	189	1 Y064.METJA	Q60376 methanococ
21	56	35.4	1046	1 POL_SIVAG	P27980 simian immu
22	54	34.2	1061	1 POL_SIVAT	P05695 simian immu
23	53	33.5	357	1 AAAA.EMENI	P21133 emericeella
24	51.5	32.6	415	1 CGA2.XENLA	P47827 xenopus lae
25	51	32.3	746	1 PCAP_HUMAN	Q96rn5 homo sapien
26	51	32.3	792	1 PCAP_MOUSE	Q924h2 mus musculu
27	50.5	32.0	741	1 RN5A_HUMAN	Q05823 homo sapien
28	48.5	30.7	452	1 TRFC_HELPY	O25867 helicobacte
29	47.5	30.1	150	1 RNK6_SAISC	O46529 saimir sci
30	47.5	30.1	154	1 RNK6_BOVIN	P08904 bos taurus
31	47	29.7	257	1 ABCX_GALVS	P35020 galdieria s
32	47	29.7	406	1 CGA2_BOVIN	P30274 bos taurus
33	47	29.7	421	1 CGA1_MOUSE	Q61456 mus musculu

RESULT 1

ID	IL2_HUMAN	STANDARD;	PRT;	153 AA.
AC	P01585;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF)			
DE	(Aldelesleukin).			
GN	IL2.			
OS	Homo sapiens (Human), and			
OS	Hylobates lar (Common gibbon).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606; 9580;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	SPECIES=Human;			
RX	MEDLINE=84247353; PubMed=6330695;			
RA	Holbrook N.J., Lieber M., Crabtree G.R.;			
RT	"DNA sequence of the 5' flanking region of the human interleukin 2			
RT	gene: homologues with adult T-cell leukemia virus.;"			
RL	Nucleic Acids Res. 12:5005-5013(1984).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	SPECIES=Human;			
RX	MEDLINE=83167472; PubMed=6403867;			
RA	Taniguchi T., Matsui H., Fujita T., Takaoka C., Kashima N.,			
RA	Yoshimoto R., Hamuro J.;			
RT	"Structure and expression of a cloned cDNA for human interleukin-2.;"			
RL	Nature 302:305-310(1983).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	SPECIES=Human;			
RX	MEDLINE=84023840; PubMed=6312994;			
RA	Maeda S., Nishino N., Obaru K., Mita S., Nomiya H., Shimada K.,			
RA	Fujimoto K., Teranishi T., Hirano T., Onoue K.;			
RT	"Cloning of interleukin 2 mRNAs from human tonsils.;"			
RL	Biochem. Biophys. Res. Commun. 115:1040-1047(1983).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	SPECIES=Human;			
RX	MEDLINE=83246551; PubMed=6306584;			
RA	Devos R., Platinck G., Cheroutre H., Simons G., Degraeve W.,			
RA	Tavernier J., Remaut E., Fiers W.;			
RT	"Molecular cloning of human interleukin 2 cDNA and its expression in			
RT	E. coli.;"			
RL	Nucleic Acids Res. 11:4307-4323(1983).			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RC	SPECIES=Human;			
RX	MEDLINE=84170356; PubMed=6608729;			
RA	Holbrook N.J., Smith K.A., Fornace A.J. Jr., Comeau C.M.,			
RA	Wiskocil R.L., Crabtree G.R.;			
RT	"T-cell growth factor: complete nucleotide sequence and organization			
RT	of the gene in normal and malignant cells.;"			

P20248 homo sapien
P78396 homo sapien
P34408 caenorhabdi
P26362 squalus aca
O75148 homo sapien
O51872 borrelia bu
P29617 drosophila
Q9cna0 pasteurella
P44583 haemophilus
P33860 saccharomyc
P34738 neurospora
O44218 drosophila

RL Proc. Natl. Acad. Sci. U.S.A. 81:1634-1638(1984).
 RN [16]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Human;
 RX MEDLINE=84170243; PubMed=6324170;
 RA Fujita T., Takaoka C., Mateui H., Taniguchi T.;
 RT "Structure of the human interleukin 2 gene.";
 RL Proc. Natl. Acad. Sci. U.S.A. 80:7437-7441(1983).
 RN [17]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Human;
 RX MEDLINE=9523150; PubMed=7722480;
 RA Eisenberg O., Faber-Elman A., Lotan M., Schwartz M.;
 RT "Interleukin-2 transcripts in human and rodent brains: possible
 expression by astrocytes.";
 RL J. Neurochem. 64:1928-1936(1995).
 RN [8]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Human;
 RX MEDLINE=96422299; PubMed=8824916;
 RA Chernicky C.L., Tan H., Burfelind P., Ilan J., Ilan J.;
 RT "Sequence of interleukin-2 isolated from human placental poly A+ RNA:
 possible role in maintenance of fetal allograft.";
 RL Mol. Reprod. Dev. 43:180-186(1996).
 RN [9]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Human;
 RX MEDLINE=96422299; PubMed=8824916;
 RA Nickerson D.A.;
 RT Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 RN [10]
 RP SEQUENCE OF 21-153 FROM N.A.
 RC SPECIES=Human;
 RX MEDLINE=89062420; PubMed=3264184;
 RA Weir M.P., Chaplin M.A., Wallace D.M., Dykes C.W., Hobden A.N.;
 RT "Structure-activity relationships of recombinant human interleukin
 2.";
 RL Biochemistry 27:6883-6892(1988).
 RN [11]
 RP SEQUENCE OF 1-69 FROM N.A.
 RC SPECIES=Human;
 RX MEDLINE=87064618; PubMed=3491296;
 RA Siebenlist U., Durand D.B., Bressler P., Holbrook N.J., Norris C.A.,
 RA Kanoun M., Kant J.A., Crabtree G.R.;
 RT "Promoter region of interleukin-2 gene undergoes chromatin structure
 changes and confers inducibility on chloramphenicol acetyltransferase
 gene during activation of T cells.";
 RL Mol. Cell. Biol. 6:3042-3049(1986).
 RN [12]
 RP SEQUENCE OF 1-68 FROM N.A.
 RC SPECIES=Human;
 RA Nishino N., Obaru K., Maeda S., Shimada K., Onoue K.;
 RT "Organization of the DNA regions flanking the human interleukin 2
 gene.";
 RL Biochem. Res. 6:197-205(1985).
 RN [13]
 RP SEQUENCE OF 21-153, DISULFIDE BOND, AND CARBOHYDRATE-LINKAGE SITE.
 RC SPECIES=Human;
 RX MEDLINE=85038540; PubMed=6333684;
 RA Robb R.J., Kutny R.M., Panico M., Morris H.R., Chowdhry V.;
 RT "Amino acid sequence and post-translational modification of human
 interleukin 2.";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:6486-6490(1984).
 RN [14]
 RP CARBOHYDRATE-LINKAGE SITE.
 RC SPECIES=Human;
 RX MEDLINE=90008901; PubMed=2793860;
 RA Conrad H.S., Nimitz M., Dittmar K.E.J., Lindenmaier W., Hoppe J.,
 RA Hauser H.;
 RT "Expression of human interleukin-2 in recombinant baby hamster
 kidney, ltk-, and Chinese hamster ovary cells. Structure of O-linked
 carbohydrate chains and their location within the polypeptide.";
 RL J. Biol. Chem. 264:17368-17373(1989).

RN [15]
 RP SEQUENCE FROM N.A.
 RC SPECIES=H.lar;
 RX MEDLINE=86042650; PubMed=3877307;
 RA Chen S.J., Holbrook N.J., Mitchell K.F., Vallone C.A.,
 RA Greengard J.S., Crabtree G.R., Lin Y.;
 RT "A viral long terminal repeat in the interleukin 2 gene of a cell
 line that constitutively produces interleukin 2.";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:7284-7288(1985).
 RN [16]
 RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
 RC SPECIES=Human;
 RX MEDLINE=88070646; PubMed=3500515;
 RA Brandhuber B.J., Boone T., Kenney W.C., McKay D.B.;
 RT "Three-dimensional structure of interleukin-2.";
 RL Science 238:1707-1709(1987).
 RN [17]
 RP X-RAY CRYSTALLOGRAPHY.
 RC SPECIES=Human;
 RX MEDLINE=92335891; PubMed=1631562;
 RA Bazan J.F.;
 RT "Unravelling the structure of IL-2.";
 RL Science 257:410-412(1992).
 RN [18]
 RP RESPONSE TO ABOVE LETTER.
 RA McKay D.B.;
 RL Science 257:412-413(1992).
 RN [19]
 RP STRUCTURE BY NMR.
 RX MEDLINE=92379010; PubMed=1510960;
 RA Mott H.R., Driscoll P.C., Boyd J., Cooke R.M., Weir M.P.,
 RA Campbell I.D.;
 RT "Secondary structure of human interleukin 2 from 3D heteronuclear NMR
 experiments.";
 RL Biochemistry 31:7741-7744(1992).
 RN [20]
 RP 3D-STRUCTURE MODELING.
 RX MEDLINE=95111955; PubMed=7529123;
 RA Bamorough P., Hedgecock C.J., Richards W.G.;
 RT "The interleukin-2 and interleukin-4 receptors studied by molecular
 modelling.";
 RL Structure 2:839-851(1994).
 CC -1- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR
 MITOGENIC STIMULATION, THIS PROTEIN IS REQUIRED FOR T-CELL
 PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE
 IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-
 ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- DISEASE: A FORM OF T-CELL ACUTE LYMPHOBLASTIC LEUKEMIA (T-ALL) IS
 CHARACTERIZED BY A CHROMOSOMAL TRANSLOCATION T(4;16)(Q26;P13)
 WHICH INVOLVES IL2 AND BCMA.
 CC -1- PHARMACEUTICAL: Available under the name Proleukin (Chiron). Used
 in patients with renal cell carcinoma or metastatic melanoma.
 CC -1- SIMILARITY: BELONGS TO THE IL-2 FAMILY.
 CC -1- DATABASE: NAME-R&D Systems' cytokine source book: IL2;
 WWW-"http://www.rndsystems.com/asp/g_sitebuilder.asp?bodyId=206".
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; J00264; AAD48509.1; -
 CC EMBL; X01586; CAA25742.1; -
 CC EMBL; V00564; CAA23827.1; -
 CC EMBL; X00695; CAA25292.1; -
 CC EMBL; K02056; AAA98792.1; -
 CC EMBL; M13879; AAA59141.1; -
 CC EMBL; K03174; AAA35453.1; -
 CC EMBL; S77834; AAD14263.2; -
 CC EMBL; S82692; AAB46883.1; -

Query Match 93.0%; Score 147; DB 1; Length 153;
Best Local Similarity 96.8%; Pred. No. 5.8e-15;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLEHLLKLQMLNGINNY 32
DB 21 APTSSSTKKTQLEHLLKLQMLNGINNY 51

RESULT 2

IL2_MACFA

ID IL2_MACFA STANDARD; PRT; 154 AA.
AC Q29615;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
GN IL2.

OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9541;
RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Peripheral blood;

RA Yabe M., Matsuura Y., Tatsumi M.;

RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR

CC MITOGENIC STIMULATION, THIS PROTEIN IS REQUIRED FOR T-CELL

CC PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE

CC IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-

CC ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS (BY

CC SIMILARITY).

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- SIMILARITY: BELONGS TO THE IL-2 FAMILY.

CC -----
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CC -----

DR EMBL; D63352; BAA09676.1; -.

DR HSSP; P01585; 3INK.

DR InterPro: IPR000779; Interleukin-2.

DR Pfam: PF00715; IL2; 1.

DR PRINTS; PR00265; INTERLEUKIN2.

DR ProDom; PD003649; Interleukin-2; 1.

DR SMART; SM00189; IL2; 1.

DR PROSITE; PS00424; INTERLEUKIN_2; 1.

KW Cytokine; Glycoprotein; Immune response; Signal; Growth factor;

KW T-cell.

FT SIGNAL. 1 20 BY SIMILARITY.

FT CHAIN. 21 154 INTERLEUKIN-2.

FT CARBOHYD. 23 23 O-LINKED (GALNAC. . .) (BY SIMILARITY).

FT DISULFID. 78 126 BY SIMILARITY.

SQ SEQUENCE 154 AA; 17686 MW; 7853FE62A5E4A49 CRC64;

Query Match 93.0%; Score 147; DB 1; Length 154;

Best Local Similarity 96.8%; Pred. No. 5.8e-15;

Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLEHLLKLQMLNGINNY 32

DB 21 APTSSSTKKTQLEHLLKLQMLNGINNY 51

RESULT 3

IL2_MACMU

IL2_MACMU STANDARD; PRT; 154 AA.

P51498;

AC 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).

GN IL2.

OS Macaca mulatta (Rhesus macaque), and

OS Macaca nemestrina (Pig-tailed macaque).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;

OC Cercopitheidae; Macaca.

OX NCBI_TaxID=9544, 9545;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Blood;

RX MEDLINE=96003435; PubMed=7561102;

RA Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;

RT "Comparative sequence analysis of cytokine genes from human and

RT nonhuman primates.";

RL J. Immunol. 155:3946-3954(1995).

CC -!- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR

CC MITOGENIC STIMULATION, THIS PROTEIN IS REQUIRED FOR T-CELL

CC PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE

CC IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-

CC ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS (BY

CC SIMILARITY).

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- SIMILARITY: BELONGS TO THE IL-2 FAMILY.

CC -----
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CC -----

DR EMBL; U19847; AAB60400.1; -.

DR EMBL; U19852; AAA86714.1; -.

DR HSSP; P01585; 3INK.

DR InterPro: IPR000779; Interleukin-2.

DR Pfam: PF00715; IL2; 1.

DR PRINTS; PR00265; INTERLEUKIN2.

DR ProDom; PD003649; Interleukin-2; 1.

DR SMART; SM00189; IL2; 1.

DR PROSITE; PS00424; INTERLEUKIN_2; 1.

KW Cytokine; Glycoprotein; Immune response; Signal; Growth factor;

KW T-cell.

FT SIGNAL. 1 20 BY SIMILARITY.

FT CHAIN. 21 154 INTERLEUKIN-2.

FT CARBOHYD. 23 23 O-LINKED (GALNAC. . .) (BY SIMILARITY).

FT DISULFID. 78 126 BY SIMILARITY.

SQ SEQUENCE 154 AA; 17685 MW; 6AEB480F204BA49 CRC64;

Query Match 93.0%; Score 147; DB 1; Length 154;

Best Local Similarity 96.8%; Pred. No. 5.8e-15;

Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLEHLLKLQMLNGINNY 32

DB 21 APTSSSTKKTQLEHLLKLQMLNGINNY 51

RESULT 4

IL2_CERTO

ID IL2_CERTO STANDARD; PRT; 154 AA.

AC P46649;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).

GN IL2.


```

RN  [3]
RP  SEQUENCE FROM N.A.
RC  STRAIN=Beagle; TISSUE=Spleen;
RX  MEDLINE=95347614; PubMed=7622066;
RA  Knapp D.W., Williams J.S., Andrisani O.M.;
RT  "Cloning of the canine interleukin-2 encoding cDNA.";
RL  Gene 159:281-282(1995).
CC  -!- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR
CC  MITOGENIC STIMULATION, THIS PROTEIN IS REQUIRED FOR T-CELL
CC  PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE
CC  IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-
CC  ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS.
CC  -!- SUBCELLULAR LOCATION: Secreted.
CC  -!- SIMILARITY: BELONGS TO THE IL-2 FAMILY.
CC  -----
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CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; D30710; BAA06378.1; -.
DR  EMBL; U28141; AA68969.1; -.
DR  EMBL; U11689; AA75360.1; -.
DR  HSSP; P01585; 3INK.
DR  InterPro; IPR000779; Interleukin-2.
DR  Pfam; PF00715; IL2; 1.
DR  PRINTS; PR00265; INTERLEUKIN2.
DR  ProDom; PD003649; Interleukin-2; 1.
DR  SMART; SM00189; IL2; 1.
DR  PROSITE; PS00424; INTERLEUKIN_2; 1.
KW  Cytokine; Glycoprotein; Immune response; Signal; Growth factor;
KW  T-cell.
FT  SIGNAL          1  20      BY SIMILARITY.
FT  CHAIN           21  155     INTERLEUKIN-2.
FT  CARBOHYD        112  112     O-LINKED (GLCNAC. . .) (BY SIMILARITY).
FT  DISULFID        79  127     BY SIMILARITY.
FT  CONFLICT        4  4       M -> I (IN REF. 3).
FT  CONFLICT        37  37     Q -> R (IN REF. 3).
FT  CONFLICT        151 151     F -> Y (IN REF. 3).
FT  CONFLICT        154 154     L -> M (IN REF. 3).
SQ  SEQUENCE 155 AA; 17668 MW; D123E486B7F4ACID CRC64;

Query Match      68.0%; Score 107.5; DB 1; Length 155;
Best Local Similarity 68.8%; Pred. No. 4.9e-09;
Matches 22; Conservative 6; Mismatches 3; Indels 1; Gaps 1;

QY  2 AP-TSSSTKKTQLQLEHLHLKQLMILGNNY 32
Db  21 APTSSSTKETEQLQLEHLHLKQLMILGNNY 52
|| |||||:|:| || |||||:|:| |||||

RESULT 7
IL2_RABIT
ID  IL2_RABIT          STANDARD;          PRT; 153 AA.
AC  Q77620;
DT  15-JUL-1999 (Rel. 38, Created)
DT  15-JUL-1999 (Rel. 38, Last sequence update)
DT  15-JUN-2002 (Rel. 41, Last annotation update)
DE  Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
GN  IL2.
OS  Oryctolagus cuniculus (Rabbit).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Euthera; Lagomorpha; Leporidae; Oryctolagus.
OX  NCBI_TaxID=9986;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  TISSUE=Lymph node;
RX  MEDLINE=20304414; PubMed=10843729;
RA  Perkins H.D., van Leeuwen B.H., Hardy C.M., Kerr P.J.;

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RT  "The complete cDNA sequences of IL-2, IL-4, IL-6 AND IL-10 from the
RL  European rabbit (Oryctolagus cuniculus).";
CC  -!- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR
CC  MITOGENIC STIMULATION, THIS PROTEIN IS REQUIRED FOR T-CELL
CC  PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE
CC  IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-
CC  ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS.
CC  -!- SUBCELLULAR LOCATION: Secreted.
CC  -!- SIMILARITY: BELONGS TO THE IL-2 FAMILY.
CC  -----
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CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; AF068057; AAC23838.1; -.
DR  HSSP; P01585; 3INK.
DR  InterPro; IPR000779; Interleukin-2.
DR  Pfam; PF00715; IL2; 1.
DR  PRINTS; PR00265; INTERLEUKIN2.
DR  ProDom; PD003649; Interleukin-2; 1.
DR  SMART; SM00189; IL2; 1.
DR  PROSITE; PS00424; INTERLEUKIN_2; 1.
KW  Cytokine; Glycoprotein; Immune response; Signal; Growth factor;
KW  T-cell.
FT  SIGNAL          1  20      BY SIMILARITY.
FT  CHAIN           21  153     INTERLEUKIN-2.
FT  CARBOHYD        23  23     O-LINKED (GLCNAC. . .) (BY SIMILARITY).
FT  DISULFID        111 111     N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD        78  125     BY SIMILARITY.
SQ  SEQUENCE 153 AA; 17256 MW; 8173536B2DD8886 CRC64;

Query Match      67.7%; Score 107; DB 1; Length 153;
Best Local Similarity 67.7%; Pred. No. 5.8e-09;
Matches 21; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY  2 APTSSSTKKTQLQLEHLHLKQLMILGNNY 32
Db  21 APTSSSTKETEQLQLEHLHLKQLMILGNNY 51
|||||||:|:| || |||||:|:| |||||

RESULT 8
IL2_FELCA
ID  IL2_FELCA          STANDARD;          PRT; 154 AA.
AC  Q07885;
DT  01-OCT-1994 (Rel. 30, Created)
DT  01-OCT-1994 (Rel. 30, Last sequence update)
DT  15-DEC-1998 (Rel. 37, Last annotation update)
DE  Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
GN  IL2.
OS  Felis silvestris catus (Cat).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Euthera; Carnivora; Fissipedia; Felidae; Felis.
OX  NCBI_TaxID=9685;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=93356765; PubMed=8352761;
RA  Cozzi P.J., Padrid P.A., Takeda J., Alegre M.-A., Yuhki N.,
RA  Leff A.R.;
RT  "Sequence and functional characterization of feline interleukin 2.";
RL  Biochem. Biophys. Res. Commun. 194:1038-1043(1993).
RN  [2]
RP  SEQUENCE FROM N.A.
RA  Litman R., Gibbs C., Good R.A., Day N.K.;
RL  Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
CC  -!- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR
CC  MITOGENIC STIMULATION, THIS PROTEIN IS REQUIRED FOR T-CELL
CC  PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE
CC  IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-

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DR EMBL: X56750; CAA40071.1; -
 DR EMBL: X58428; CAA41330.1; -
 DR EMBL: AB041935; BAB16110.1; -
 DR PIR: S15473; S15473.
 DR PIR: S16241; S16241.
 DR HSSP: P01585; 3INK.

DR InterPro: IPR000779; Interleukin-2.
 DR Pfam: PF00715; IL2; 1.
 DR PRINTS: PR00265; INTERLEUKIN2.
 DR ProDom: PD003649; Interleukin-2; 1.
 DR SMART: SM00189; IL2; 1.
 DR PROSITE: PS00424; INTERLEUKIN_2; 1.

KW Cytokine; Glycoprotein; Immune response; Signal; Growth factor;
 KW T-cell.

FT SIGNAL 1 20 BY SIMILARITY.
 FT CHAIN 21 154 INTERLEUKIN-2.
 FT CARBOHYD 23 23 O-LINKED (GALNAC. . .) (BY SIMILARITY).
 FT DISULFID 78 126 BY SIMILARITY.
 SQ SEQUENCE 154 AA; 17401 MW; F3B95E43D4A3D3E1 CRC64;

Query Match 60.8%; Score 96; DB 1; Length 154;
 Best Local Similarity 64.5%; Pred. No. 2.6e-07;
 Matches 20; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 2 APTSSSTKTKTQLEHLLKQLMILGINNY 32
 DB 21 APTSSSTKTKTQLEHLLKQLMILGINNY 51

RESULT 11
 IL2_MERUN
 ID IL2_MERUN STANDARD; PRT; 155 AA.

AC Q08081;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
 GN IL2.

OS Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
 CC Meriones.

CC NCBI_TaxID=10047;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RX MEDLINE=94174702; PubMed=8128610;

RA Mai Z., Kousoulas K.G., Horohov D.W., Klei T.R.;
 RT "Cross-species PCR cloning of gerbil (Meriones unguiculatus)
 RT Interleukin-2 cDNA and its expression in COS-7 cells.";
 RL Vet. Immunol. Immunopathol. 40:63-71(1994).

CC -!- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR
 CC MITOGENIC STIMULATION, THIS PROTEIN IS REQUIRED FOR T-CELL
 CC PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE
 CC IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-
 CC ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- SIMILARITY: BELONGS TO THE IL-2 FAMILY.

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DR EMBL: X68779; CAA48679.1; -

DR PIR: S33509; S33509.
 DR HSSP: P01585; 3INK.

DR InterPro: IPR000779; Interleukin-2.
 DR Pfam: PF00715; IL2; 1.
 DR PRINTS: PR00265; INTERLEUKIN2.
 DR ProDom: PD003649; Interleukin-2; 1.
 DR SMART: SM00189; IL2; 1.
 DR PROSITE: PS00424; INTERLEUKIN_2; 1.

KW Cytokine; Glycoprotein; Immune response; Signal; Growth factor;
 KW T-cell.

FT SIGNAL 1 20 BY SIMILARITY.
 FT CHAIN 21 155 INTERLEUKIN-2.
 FT CARBOHYD 23 23 O-LINKED (GALNAC. . .) (BY SIMILARITY).
 FT DISULFID 78 126 BY SIMILARITY.
 SQ SEQUENCE 155 AA; 17602 MW; D0F74AALA381CDDA CRC64;

Query Match 60.1%; Score 95; DB 1; Length 155;
 Best Local Similarity 64.5%; Pred. No. 3.7e-07;
 Matches 20; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

QY 2 APTSSSTKTKTQLEHLLKQLMILGINNY 32
 DB 21 APTSSPAKEAQYLEQLLDLQQLRGINNY 51

RESULT 12
 IL2_ORCOR
 ID IL2_ORCOR STANDARD; PRT; 152 AA.

AC Q97513;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF)
 DE (Fragment).
 GN IL2.

OS Orcinus orca (Killer whale).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae;
 CC Orcinus.

CC NCBI_TaxID=9733;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ness T.L., Bradley W.G., Reynolds J.E. III, Roess W.B.;

RT "Isolation and expression of the interleukin-2 gene from the killer
 RT whale, Orcinus orca.";
 RL Mar. Mamm. Sci. 14:531-543(1998).

CC -!- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR
 CC MITOGENIC STIMULATION, THIS PROTEIN IS REQUIRED FOR T-CELL
 CC PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE
 CC IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-
 CC ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS (BY
 CC SIMILARITY).

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- SIMILARITY: BELONGS TO THE IL-2 FAMILY.

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 CC or send an email to license@isb-sib.ch).

DR EMBL: AF009570; AAD01426.1; -

DR HSSP: P01585; 1IBL.

DR InterPro: IPR000779; Interleukin-2.

DR Pfam: PF00715; IL2; 1.

DR PRINTS: PR00265; INTERLEUKIN2.

DR ProDom: PD003649; Interleukin-2; 1.
 DR SMART: SM00189; IL2; 1.
 DR PROSITE: PS00424; INTERLEUKIN_2; 1.

KW Cytokine; Glycoprotein; Immune response; Signal; Growth factor;
 KW T-cell.

FT	SIGNAL	1	20	BY SIMILARITY.
FT	CHAIN	21	>152	INTERLEUKIN-2.
FT	CARBOHYD	23	23	O-LINKED (GALNAC. . .) (BY SIMILARITY).
FT	DISULFID	78	126	BY SIMILARITY.
FT	NON_TER	152	152	
SQ	SEQUENCE	152 AA;	17424 MW;	308F91821ECCB764 CRC64;

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RESULT 13
IL2_HORSE      STANDARD;      PRT;      149 AA.
ID             AC              DT
IL2_HORSE      P37997;
AC              DT
P1-OCT-1994 (Rel. 30, Created)
11-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
IL2.
DE              DT
EQUUS caballus (Horse).
OS              DT
Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC              DT
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX              DT
NCBI_TaxID=9796;
[1]
SEQUENCE FROM N.A.
RP              DT
MEDLINE=941160538; PubMed=8116217;
RA              DT
Vandergriff E.V., Horohov D.W.;
RT              DT
"Molecular cloning and expression of equine interleukin 2.";
RL              DT
Vet. Immunol. Immunopathol. 39:395-406(1993).
[2]
SEQUENCE FROM N.A.
RP              DT
Tavernor A.S., Allen W.R., Butcher G.W.;
RA              DT
Submitted (NOV-1992) to the EMBL/GenBank/DBJ databases.
RL              DT
-1- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR
CC              DT
MITOGENIC STIMULATION, THIS PROTEIN IS REQUIRED FOR T-CELL
CC              DT
PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE
CC              DT
IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-
CC              DT
ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS.
CC              DT
-1- SUBCELLULAR LOCATION: Secreted.
CC              DT
-1- SIMILARITY: BELONGS TO THE IL-2 FAMILY.
CC              DT
-----
CC              DT
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CC              DT
or send an email to license@isb-sib.ch).
CC              DT
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CC              DT
EMBL; L06009; AAA20134.1; -.
CC              DT
EMBL; X69393; CAA49190.1; -.
CC              DT
PIR; S31391; S31391.
CC              DT
HSP; P01585; 3INK.
CC              DT
InterPro; IPR000779; Interleukin-2.
CC              DT
Pfam; PF00715; IL2; 1.
CC              DT
PRINTS; P00265; INTERLEUKIN2.
CC              DT
ProDom; PD003649; Interleukin-2; 1.
CC              DT
SMART; SM00189; IL2; 1.
CC              DT
PROSITE; PS00424; INTERLEUKIN_2; 1.
CC              DT
Cytokine; Glycoprotein; Immune response; Signal; Growth factor;
CC              DT
T-cell.
CC              DT
-----
CC              DT
SIGNAL          1 20 BY SIMILARITY.
CC              DT
CHAIN           21 149 INTERLEUKIN-2.
CC              DT
DISULFID        78 121 BY SIMILARITY.
CC              DT
FT CARBOHYD     23 23 O-LINKED (GLNAC. . .) (BY SIMILARITY).
CC              DT
FT CARBOHYD    106 106 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC              DT
FT CONFLICT     3 3 R -> K (IN REF. 2).

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FT CONFLICT      8      8      S -> A (IN REF. 2).
FT CONFLICT     59     59     I -> M (IN REF. 2).
FT CONFLICT    125    125     N -> D (IN REF. 2).
FT CONFLICT    128    128     E -> G (IN REF. 2).
FT CONFLICT    145    145     I -> F (IN REF. 2).
FT CONFLICT    148    148     L -> M (IN REF. 2).
SQ SEQUENCE    149 AA; 17086 MW; 051BB8C47A0114FC CRC64;

Query Match      53.8%; Score 85; DB 1; Length 149;
Best Local Similarity 53.3%; Pred.No. 1.1e-05;
Matches 16; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 2 APTSSSTKTKQLQLHLLKLQMLINGNN 31
   ||||| :||| :||| :|::| :|||
Db 21 APTSSSRKTEQQQLKQLQMDLKLLEGVNN 50

RESULT 14
IL2_BOVIN
ID IL2_BOVIN STANDARD; PRT; 155 AA.
AC P05016;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
IL2 OR IL-2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
[1]
SEQUENCE FROM N.A.
MEDLINE=86205869; PubMed=3517854;
RX Carrecci D.P., McKereghan K., Larsen A., Cantrell M.A., Anderson D.,
RX Gillis S., Cosman D., Baker P.E.;
RT "Cloning, sequence, and expression of bovine interleukin 2.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:3223-3227(1986).
[2]
SEQUENCE FROM N.A.
MEDLINE=86205870; PubMed=3486415;
RX Reeves R., Spies A.G., Nissen M.S., Buck C.D., Weinberg A.D.,
RX Barr P.J., Magnuson N.S., Magnuson J.A.;
RT "Molecular cloning of a functional bovine interleukin 2 cDNA.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:3228-3232(1986).
[3]
SEQUENCE OF 1-22 FROM N.A.
TISSUE=Thymus;
RA Anikeeva N.N., Vinogradova T.V., Votoshin O.N.;
RA Submitted (DEC-1989), to the EMBL/GenBank/DBJ databases
RL CC
CC -1- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR
CC MITOGENIC STIMULATION, THIS PROTEIN IS REQUIRED FOR T-CELL
CC PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE
CC IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-
CC ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE IL-2 FAMILY.
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EMBL; M12791; AAA30586.1; -.
DR EMBL; M13204; AAA21143.1; ALT_INIT.
DR EMBL; X17201; CAA35062.1; -.
DR EMBL; X32687; CAA36912.1; -.
DR HSP; P01585; 3INK.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.

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DR PRINTS; PR00265; INTERLEUKIN2.
 DR ProDom; PD003649; Interleukin-2; 1.
 DR SMART; SM00189; IL2; 1.
 DR PROSITE; PS00424; INTERLEUKIN_2; 1.
 KW Cytokine; Glycoprotein; Immune response; Signal; Growth factor;
 KW T-cell.

FT SIGNAL 1 20 BY SIMILARITY.
 FT CHAIN 21 155 INTERLEUKIN-2.
 FT CARBOHYD 79 127 BY SIMILARITY.
 FT DISULFID 23 23 O-LINKED (GALNAC. . .) (BY SIMILARITY).
 FT CARBOHYD 23 23
 FT CONFLICT 66 66 V -> A (IN REF. 2).
 SQ SEQUENCE 155 AA; 17627 MW; 816667DFEA052EDF CRC64;

Query Match 45.6%; Score 72; DB 1; Length 155;
 Best Local Similarity 50.0%; Pred. No. 0.001;
 Matches 15; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLQLEHLLKLQMLNGINN 31
 DB 21 APTSSSTGMTKEVKSLLDLQLLEKVRN 50

RESULT 15

IL2_CAPHI
 ID IL2_CAPHI STANDARD; PRT; 155 AA.
 AC P36835; P79156;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
 GN IL2.
 OS Capra hircus (Goat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Capra.
 OX NCBI_TaxID=9925;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RA Rimstad E.;
 RL Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Beyer J.C.; Cheevers W.P.;
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR
 CC MITOGENIC STIMULATION, THIS PROTEIN IS REQUIRED FOR T-CELL
 CC PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE
 CC IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-
 CC ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE IL-2 FAMILY.

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DR EMBL; X76063; CAA53664.1; .
 DR EMBL; U34274; AAB38527.1; .
 DR PIR; S38662; S38662.
 DR HSP; P01585; 3INK.
 DR InterPro; IPR000779; Interleukin-2.
 DR Pfam; PF00715; IL2; 1.
 DR PRINTS; PR00265; INTERLEUKIN2.
 DR ProDom; PD003649; Interleukin-2; 1.
 DR SMART; SM00189; IL2; 1.
 DR PROSITE; PS00424; INTERLEUKIN_2; 1.
 KW Cytokine; Glycoprotein; Immune response; Signal; Growth factor;
 KW T-cell.

FT SIGNAL 1 20 BY SIMILARITY.
 FT CHAIN 21 155 INTERLEUKIN-2.
 FT CARBOHYD 23 23 O-LINKED (GALNAC. . .) (BY SIMILARITY).
 FT DISULFID 79 127 BY SIMILARITY.
 FT CONFLICT 3 5 RMQ -> QIP (IN REF. 2).
 FT CONFLICT 22 22 P -> T (IN REF. 2).
 FT CONFLICT 30 30 T -> P (IN REF. 2).
 FT CONFLICT 51 51 L -> P (IN REF. 2).
 FT CONFLICT 71 71 D -> A (IN REF. 2).
 FT CONFLICT 89 89 D -> E (IN REF. 2).
 FT CONFLICT 99 99 R -> L (IN REF. 2).
 FT CONFLICT 107 113 YNASLKG -> SMDNIKR (IN REF. 2).
 FT CONFLICT 140 140 Q -> L (IN REF. 2).
 FT CONFLICT 144 144 T -> I (IN REF. 2).
 FT CONFLICT 154 154 L -> M (IN REF. 2).
 SQ SEQUENCE 155 AA; 17703 MW; 90022DFBB6AF78DE CRC64;

Query Match 45.6%; Score 72; DB 1; Length 155;
 Best Local Similarity 50.0%; Pred. No. 0.001;
 Matches 15; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLQLEHLLKLQMLNGINN 31
 DB 21 APTSSSTGMTKEVKSLLDLQLLEKVRN 50

Search completed: February 20, 2003, 10:05:24
 Job time : 8.11111 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 20, 2003, 10:03:07 ; Search time 24.8889 Seconds
(without alignments)
264.918 Million cell updates/sec

Title: US-09-776-781-6
Perfect score: 158
Sequence: 1 MAPSSSTKKTQLQLEHLLKQLMILGINNY 32

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
-13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	147	93.0	150	4 Q9C001	Q9C001 homo sapien
2	145	91.8	154	6 Q9XS38	Q9XS38 papio hamad
3	135.5	85.8	156	4 Q13169	Q13169 homo sapien
4	134	84.8	139	4 Q16334	Q16334 homo sapien
5	108.5	68.7	155	6 Q9XTB3	Q9XTB3 halichoerus
6	107.5	68.0	66	6 Q9BG74	Q9BG74 canis famil
7	107	67.7	79	6 Q9TV12	Q9TV12 canis famil
8	106	67.1	155	11 Q923T2	Q923T2 sigmodon hi
9	103	65.2	138	11 Q70329	Q70329 mesocricetu
10	99	62.7	133	6 Q9MZ93	Q9MZ93 oryctolagus
11	84	53.2	23	4 Q9UCF5	Q9UCF5 homo sapien
12	78	49.4	154	6 Q9XT84	Q9XT84 delphinapte
13	75	47.5	152	11 Q88210	Q88210 cavia porce
14	72	45.6	69	6 Q9GJ84	Q9GJ84 ovis aries
15	72	45.6	155	6 Q9GL83	Q9GL83 capra hircu
16	72	45.6	155	6 Q95KP3	Q95KP3 bubalus bub

17 69 43.7 39 6 Q9BG73
18 69 43.7 150 11 P70291
19 69 43.7 169 11 Q9QUS8
20 67 42.4 150 11 P70294
21 65.5 41.5 155 11 P70292
22 62.5 39.6 159 11 P70293
23 56 35.4 300 2 Q8VW37
24 56 35.4 348 12 Q9DHS6
25 53 33.5 251 12 Q9PYU2
26 53 33.5 452 10 Q9ZV75
27 52 32.9 116 6 Q29138
28 52 32.9 478 17 Q8TLR6
29 51 32.3 517 16 Q8R6R8
30 51 32.3 737 16 Q9KTS5
31 51 32.3 866 16 Q25517
32 51 32.3 875 16 Q9ZKZ8
33 50 31.6 95 2 Q9F8U6
34 50 31.6 304 16 Q930K5
35 50 31.6 543 16 Q9KSF8
36 49.5 31.3 104 10 Q9FSQ4
37 49.5 31.3 367 10 Q9SIF5
38 49.5 31.3 474 10 Q06376
39 49 31.0 145 16 Q9KAW0
40 48.5 30.7 288 16 Q99TY7
41 48.5 30.7 366 16 Q98422
42 48 30.4 311 16 Q9CLL6
43 48 30.4 398 16 Q50911
44 48 30.4 441 16 Q928V0
45 48 30.4 441 16 Q69192

ALIGNMENTS

RESULT 1

ID Q9C001 PRELIMINARY; PRT; 150 AA.
AC Q9C001;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Interleukin-2 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-20545237; PubMed-11093171;
RA Matesanz F., Delgado C., Fresno M., Alcina A.;
RT "Allelic selection of human IL-2 gene."
RL Eur. J. Immunol. 30:3516-3521(2000).
DR EMBL; AF228636; AAG53575.1; -
DR HSSP; P01585; 3INK.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00265; INTERLEUKIN2.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
FT NON_TER 150 150
SQ SEQUENCE 150 AA; 17312 MW; BF25860F8436ACE5 CRC64;

Query Match 93.0%; Score 147; DB 4; Length 150;
Best Local Similarity 96.8%; Pred. No. 4.2e-14;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLQLEHLLKQLMILGINNY 32

Db 21 APTSSSTKKTQLQLEHLLKQLMILGINNY 51

RESULT 2

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Q9XS38
ID Q9XS38 PRELIMINARY; PRT; 154 AA.
AC Q9XS38;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
DE IL-2.
OS Papio hamadryas (Hamadryas baboon),
OS Aotus lemurinus (Northern gray-necked night monkey),
OS Aotus nancymae (Owl monkey),
OS Aotus nigriceps (black-headed night monkey), and
OS Aotus vociferans (noisy night monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Papio.
OX NCBI_TaxID=9557, 43147, 37293, 57175, 57176;
RN [1]
RP SEQUENCE FROM N.A.
RA Murillo L.A., Hernandez E., Echeverry S.J., Mendez J.A., Moreno A.,
RA Patatroyo M.E.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U88365; AAD41538.1; -
DR EMBL; U88364; AAD41534.1; -
DR EMBL; U88361; AAD41535.1; -
DR EMBL; U88363; AAD41536.1; -
DR EMBL; U88362; AAD41537.1; -
DR HSSP; P01585; 3INK.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00265; INTERLEUKIN2.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
SQ SEQUENCE 154 AA; 17675 MW; AB752ABBADA96469 CRC64;

Query Match 91.8%; Score 145; DB 6; Length 154;
Best Local Similarity 93.5%; Pred. No. 8.5e-14;
Matches 29; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 APTSSSTKTKTQLQLEHLLKLQMLINGINNY 32
| | | | | | | | | | | | | | | | | | | | | |
Db 21 APTSSSTKTKTQLQLEHLLKLQMLINGINNY 51

RESULT 3
Q13169 PRELIMINARY; PRT; 156 AA.
AC Q13169;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Interleukin 2.
GN IL2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Xu D., Wu Y., Chen J., Yu L., Zhong M., Hui Y., Qu H.;
RT "Expression of human IL-2 from gene transferred mouse melanoma cells
RT and its effect on the growth of mouse melanoma.";
RL Chung-Hua Min Kuo Wei Sheng Wu Chi Mien I Hsueh Tsa Chih
RL 13:78-82(1993).
RN [2]
RP SEQUENCE FROM N.A.
RA Xu L.;
RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
RL EMBL; U25676; AAA70092.1; -
DR HSSP; P01585; 3INK.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00265; INTERLEUKIN2.

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DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
SQ SEQUENCE 156 AA; 18002 MW; 8E0452D43B336389 CRC64;

Query Match 85.8%; Score 135.5; DB 4; Length 156;
Best Local Similarity 88.2%; Pred. No. 2.3e-12;
Matches 30; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

QY 2 APTSSS---TKKTKQLQLEHLLKLQMLINGINNY 32
| | | | | | | | | | | | | | | | | | | | | |
Db 21 APTSSSTKTKTKTQLQLEHLLKLQMLINGINNY 54

RESULT 4
Q16334 PRELIMINARY; PRT; 139 AA.
ID Q16334;
AC Q16334;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
DE IL-2 protein (Fragment).
GN IL-2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-95239150; PubMed-7722480;
RA Eizenberg O., Faber-Elman A., Lotan M., Schwartz M.;
RT "Interleukin-2 transcripts in human and rodent brains: possible
RT expression by astrocytes.";
RL J. Neurochem. 64:1928-1936(1995).
DR EMBL; S77835; AAD14264.1; -
DR HSSP; P01585; 3INK.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00265; INTERLEUKIN2.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
FT NON_TER
SQ SEQUENCE 139 AA; 15986 MW; 731FBA406D0C63C5 CRC64;

Query Match 84.8%; Score 134; DB 4; Length 139;
Best Local Similarity 90.3%; Pred. No. 3.4e-12;
Matches 28; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 APTSSSTKTKTQLQLEHLLKLQMLINGINNY 32
| | | | | | | | | | | | | | | | | | | | | |
Db 17 APTSSSTKTKTQLQLEHLLKLQMLINGINNY 47

RESULT 5
Q9XT83 PRELIMINARY; PRT; 155 AA.
ID Q9XT83;
AC Q9XT83;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Interleukin 2.
OS Halichoerus grypus (Gray seal).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Pinnipedia; Phocidae; Halichoerus.
OX NCBI_TaxID=9711;
RN [1]
RP SEQUENCE FROM N.A.
RA St-Laurent G., Bellevue C., Archambault D.;
RT "Molecular cloning and phylogenetic analysis of beluga whale
RT (Delphinapterus leucas) and grey seal (Halichoerus grypus) interleukin
RT 2.";

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```
RC TISSUE-SPLEEN;
RX MEDLINE-98234044; PubMed-95731100;
RA Melby P.C., Tryon V.V., Chandrasekar B., Freeman G.L.;
RT "Cloning of Syrian hamster (Mesocricetus auratus) cytokine cDNAs and
RT analysis of cytokine mRNA expression in experimental visceral
RT leishmaniasis.";
RL Infect. Immun. 66:2135-2142(1998).
DR EMBL; AF046212; AAC40097.1; -.
DR HSSP; P01585; 3INK.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00265; INTERLEUKIN2.
DR PRODOM; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
FT NON_TER 1
FT NON_TER 138
SQ SEQUENCE 138 AA; 15739 MW; 3510329958670779 CRC64;

Query Match 65.2%; Score 103; DB 11; Length 138;
Best Local Similarity 71.0%; Pred. No. 1.4e-07;
Matches 22; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLQLEHLLKLQMLNGINNY 32
DB 14 APTSSSKKETQHLQQLLDLQELKGINNY 44

RESULT 10
Q9WZ99 PRELIMINARY; PRT; 133 AA.
ID Q9WZ99
AC Q9WZ99
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Interleukin 2 variant ILdelta2.
GN IL-2.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-SPLEEN, AND LYMPH NODE;
RX MEDLINE-2030414; PubMed-10843729;
RA Perkins H.D., van Leeuwen B.H., Hardy C.M., Kerr P.J.;
RT "The complete cDNA sequences of IL-2, IL-4, IL-6 and IL-10 from the
RT European rabbit (Oryctolagus cuniculus).";
RL Cytokine 12:555-565(2000).
DR EMBL; AF169168; AAF86652.1; -.
DR HSSP; P01585; 3INK.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRODOM; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
SQ SEQUENCE 133 AA; 14748 MW; 0D54758C190B5655 CRC64;

Query Match 62.7%; Score 99; DB 6; Length 133;
Best Local Similarity 69.0%; Pred. No. 5.5e-07;
Matches 20; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLQLEHLLKLQMLNGIN 30
DB 21 APTSSSTKETQQLDQLLDLQVLLKGVN 49

RESULT 11
Q9UCF5 PRELIMINARY; PRT; 23 AA.
ID Q9UCF5
AC Q9UCF5
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
OS Cavia porcellus (Guinea pig).
```

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DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Interleukin 2 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE-93289963; PubMed-8512072;
RA Mullner S., Karbe-Thonges B., Tripler D.;
RT "Charge heterogeneity of insulin fusion proteins expressed in
RT Escherichia coli is not due to proteolytic degradation.";
RL Anal. Biochem. 210:366-373(1993).
SQ SEQUENCE 23 AA; 2637 MW; 40B64C6875CE021F CRC64;

Query Match 53.2%; Score 84; DB 4; Length 23;
Best Local Similarity 85.7%; Pred. No. 1.7e-05;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 TSSTSKTKTQLQLEHLLKLQML 24
DB 3 TSXSTKTKTQLQLEHLLKLQML 23

RESULT 12
Q9XT84 PRELIMINARY; PRT; 154 AA.
ID Q9XT84
AC Q9XT84
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Interleukin 2.
OS Delphinapterus leucas (Beluga whale).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti;
OC Monodontidae; Delphinapterus.
OX NCBI_TaxID=9749;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-99221046; PubMed-10206205;
RA St-Laurent G., Belliveau C., Archambault D.;
RT "Molecular cloning and phylogenetic analysis of beluga whale
RT (Delphinapterus leucas) and grey seal (Halichoerus grypus) Interleukin
RT 2.";
RL Vet. Immunol. Immunopathol. 67:385-394(1999).
DR EMBL; AF072870; RAD40847.1; -.
DR HSSP; P01585; 3INK.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00265; INTERLEUKIN2.
DR PRODOM; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
SQ SEQUENCE 154 AA; 17652 MW; 4288D3D41D04F172 CRC64;

Query Match 49.4%; Score 78; DB 6; Length 154;
Best Local Similarity 51.6%; Pred. No. 0.00088;
Matches 16; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 2 APTSSSTKTKTQLQLEHLLKLQMLNGINNY 32
DB 21 APTSSSTENTKKQVSLQDLHLLKEINNH 51

RESULT 13
O88210 PRELIMINARY; PRT; 152 AA.
ID O88210
AC O88210;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE Interleukin 2 precursor.
OS Cavia porcellus (Guinea pig).
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
 OX NCBI_TaxID=10141;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=SPLEEN;

RA Takeyoshi M., Iwata H., Inoue T.;

RT "Guinea pig Interleukin 2(IL-2) precursor.";

RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB010093; BAA31346.1; -

DR HSSP; P01585; 11RL.

DR InterPro; IPR000779; Interleukin-2.

DR Pfam; PF00715; IL2; 1.

DR PRINTS; PR00265; INTERLEUKIN2.

DR ProDom; PD003649; Interleukin-2; 1.

DR SMART; SM00189; IL2; 1.

KW Signal.

FT SIGNAL 1 20 POTENTIAL.

FT CHAIN 21 152 INTERLEUKIN 2.

SQ SEQUENCE 152 AA; 17271 MW; CA7AC08C1B8DD1FA CRC64;

Query Match 47.5%; Score 75; DB 11; Length 152;

Best Local Similarity 56.7%; Pred. No. 0.0024;

Matches 17; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLEHLLKLQMLNGINN 31

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DB 21 APTSSSPKQTQDRLELLRLDQLTLEGVTS 50

RESULT 14

Q9GJR4

ID Q9GJR4 PRELIMINARY; PRT; 69 AA.

AC Q9GJR4;

DT 01-MAR-2001 (TREMBLrel. 16, Created)

DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE Interleukin 2 precursor (Fragment).

GN IL-2.

OS Ovis aries (Sheep).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;

OC Bovidae; Caprinae; Ovis.

OX NCBI_TaxID=9940;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=SHEEP 2, AND SHEEP 1;

RA Luehken G., Prinzenberg E.-M., Hiendleder S., Erhardt G.;

RT "A single strand conformation polymorphism in the ovine interleukin 2

(IL-2) gene.";

RL J. Anim. Sci. 0:0-0(2000).

DR EMBL; AF215687; AAG43986.1; -

DR EMBL; AF213883; AAG35709.1; -

DR HSSP; P01585; 11RL.

DR InterPro; IPR000779; Interleukin-2.

DR Pfam; PF00715; IL2; 1.

DR PRINTS; PR00265; INTERLEUKIN2.

DR ProDom; PD003649; Interleukin-2; 1.

DR SMART; SM00189; IL2; 1.

KW Signal.

FT SIGNAL 1 21 POTENTIAL.

FT CHAIN 22 >69 INTERLEUKIN 2.

FT NON_TER 69 69

SQ SEQUENCE 69 AA; 7711 MW; B8768C23BB34D1AE CRC64;

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Best Local Similarity 45.6%; Score 72; DB 6; Length 69;

Matches 15; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLEHLLKLQMLNGINN 31

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DB 21 APTSSSTGNTMKVKSLLDLQLLLEKVN 50

RESULT 15

Q9GL83

ID Q9GL83 PRELIMINARY; PRT; 155 AA.

AC Q9GL83;

DT 01-MAR-2001 (TREMBLrel. 16, Created)

DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE Interleukin 2.

GN IL-2.

OS Capra hircus (Goat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;

OC Bovidae; Caprinae; Capra.

OX NCBI_TaxID=9925;

RN [1]

RP SEQUENCE FROM N.A.

RA Ying Q.H., Li X.R., Pan J.Y.;

RT "Cloning of the goat IL-2 gene and its expression in E.coli.";

RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF307018; AAG28783.1; -

DR HSSP; P01585; 31NK.

DR InterPro; IPR000779; Interleukin-2.

DR Pfam; PF00715; IL2; 1.

DR PRINTS; PR00265; INTERLEUKIN2.

DR ProDom; PD003649; Interleukin-2; 1.

DR SMART; SM00189; IL2; 1.

DR PROSITE; PS00424; INTERLEUKIN_2; 1.

SQ SEQUENCE 155 AA; 17605 MW; EEEB2DE18F5469AA CRC64;

Query Match

Best Local Similarity 45.6%; Score 72; DB 6; Length 155;

Matches 15; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

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DB 21 APTSSSTGNTMKVKSLLDLQLLLEKVN 50

Search completed: February 20, 2003, 10:06:21

Job time : 26.8889 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 20, 2003, 10:05:07 ; Search time 8.12698 Seconds
(without alignments)
100.599 Million cell updates/sec

Title: US-09-776-781-6
Perfect score: 158
Sequence: 1 MAPSSSTKKTQLQLEHLLKLQMLINGINNY 32

Scoring table: BIOSUM62
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Searched: 140259 seqs, 2554876 residues

Total number of hits satisfying chosen parameters: 140259

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Published_Applications_AA:*
- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB pep.*
 - 2: /cgn2_6/ptodata/1/pubpaa/PCCT_NEW_PUB pep.*
 - 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB pep.*
 - 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB pep.*
 - 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB pep.*
 - 6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB pep.*
 - 7: /cgn2_6/ptodata/1/pubpaa/PCRTUS_PUBCOMB pep.*
 - 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB pep.*
 - 9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB pep.*
 - 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB pep.*
 - 11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB pep.*
 - 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB pep.*
 - 13: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB pep.*
 - 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	149	94.3	381	10	US-09-822-698A-5	Sequence 5, Appli
2	147	93.0	133	9	US-10-051-657A-1	Sequence 1, Appli
3	147	93.0	133	10	US-09-766-543-8	Sequence 8, Appli
4	147	93.0	153	10	US-09-149-721-3	Sequence 3, Appli
5	147	93.0	153	10	US-09-923-246-111	Sequence 11, App
6	143	90.5	133	10	US-09-766-543-14	Sequence 14, Appl
7	143	90.5	331	10	US-09-033-525-2	Sequence 2, Appli
8	57	36.1	43	10	US-09-835-147-11	Sequence 11, Appl
9	57	36.1	454	10	US-09-835-147-6	Sequence 6, Appli
10	57	36.1	478	10	US-09-835-147-8	Sequence 8, Appli
11	57	36.1	487	10	US-09-835-147-26	Sequence 26, Appl
12	51	32.3	751	10	US-09-881-752A-280	Sequence 280, App
13	51	32.3	866	10	US-09-815-242-11373	Sequence 11373, A
14	50	31.6	37	9	US-10-142-120-1	Sequence 1, Appli
15	47	29.7	256	9	US-09-796-149-5	Sequence 5, Appli
16	47	29.7	256	9	US-10-013-379-25	Sequence 25, Appl
17	47	29.7	515	10	US-09-925-300-1285	Sequence 1285, Ap
18	46	29.1	1403	9	US-10-108-605-93	Sequence 93, Appl
19	44	27.8	284	10	US-09-810-997-1	Sequence 1, Appli

20	44	27.8	1230	10	US-09-881-752A-150	Sequence 150, App
21	43.5	27.5	84	10	US-09-864-761-36104	Sequence 36104, A
22	43.5	27.5	908	10	US-09-895-072-15	Sequence 15, Appl
23	43.5	27.5	908	10	US-09-886-552-15	Sequence 15, Appl
24	43.5	27.5	928	10	US-09-895-072-1	Sequence 1, Appli
25	43.5	27.5	928	10	US-09-886-552-1	Sequence 1, Appli
26	43	27.2	248	10	US-09-848-294-10	Sequence 10, Appl
27	43	27.2	309	10	US-09-788-626-12	Sequence 12, Appl
28	43	27.2	421	10	US-09-841-132-577	Sequence 577, App
29	43	27.2	473	10	US-09-835-147-29	Sequence 29, Appl
30	43	27.2	556	9	US-10-012-896-1005	Sequence 1005, Ap
31	43	27.2	944	9	US-10-029-180-26	Sequence 26, Appl
32	43	27.2	990	12	US-10-047-676A-7	Sequence 7, Appli
33	43	27.2	1034	10	US-09-815-242-10331	Sequence 10331, A
34	42.5	26.9	495	9	US-10-072-094-95	Sequence 95, Appl
35	42.5	26.9	590	9	US-10-072-094-99	Sequence 99, Appl
36	42.5	26.9	780	9	US-10-072-094-93	Sequence 93, Appl
37	42.5	26.9	879	9	US-10-072-094-90	Sequence 90, Appl
38	42.5	26.9	1011	9	US-10-072-094-89	Sequence 89, Appl
39	42.5	26.9	1069	9	US-10-072-094-87	Sequence 87, Appl
40	42.5	26.9	1145	9	US-09-866-557A-5	Sequence 5, Appli
41	42	26.6	45	10	US-09-864-761-43127	Sequence 43127, A
42	42	26.6	131	9	US-09-975-719-263	Sequence 263, App
43	42	26.6	214	10	US-09-925-300-1589	Sequence 1589, Ap
44	42	26.6	529	10	US-09-815-242-13935	Sequence 13935, A
45	42	26.6	672	9	US-10-010-920-31	Sequence 31, Appl

ALIGNMENTS

RESULT 1
US-09-822-698A-5
; Sequence 5, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 5
; LENGTH: 381
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: MUC1-specific immunocytokine blvPH1-IL-2
US-09-822-698A-5

Query Match 94.3%; Score 149; DB 10; Length 381;
Best Local Similarity 93.8%; Pred. No. 6.2e-15;
Matches 30; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MAPSSSTKKTQLQLEHLLKLQMLINGINNY 32
DB 248 LAPSSSTKKTQLQLEHLLKLQMLINGINNY 279
RESULT 2
US-10-051-657A-1
; Sequence 1, Application US/10051657A
; Patent No. US20020164300A1
; GENERAL INFORMATION:
; APPLICANT: Chan, Sham-Yuen
; APPLICANT: Kelly, Ruth
; TITLE OF INVENTION: Interleukin-2 Mutein Expressed from Mammalian Cells
; FILE REFERENCE: MSB-7257
; CURRENT APPLICATION NUMBER: US/10/051,657A

; CURRENT FILING DATE: 2002-04-29
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-051-657A-1

Query Match 93.0%; Score 147; DB 9; Length 133;
Best Local Similarity 96.8%; Pred. No. 3.5e-15;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLQLEHLLKLQMLNGINNY 32
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DB 1 APTSSSTKKTQLQLEHLLKLQMLNGINNY 31

RESULT 3
US-09-766-543-8
; Sequence 8, Application US/09766543
; Patent No. US20020041865A1
; GENERAL INFORMATION:
; APPLICANT: Austin, Richard
; APPLICANT: Kwok, Cheuk S.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: METHODS FOR TREATING TUMORS
; FILE REFERENCE: PP01679.002
; CURRENT APPLICATION NUMBER: US/09/766,543
; CURRENT FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: 60/177,258
; PRIOR FILING DATE: 2000-01-20
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: human IL-2
US-09-766-543-8

Query Match 93.0%; Score 147; DB 10; Length 133;
Best Local Similarity 96.8%; Pred. No. 3.5e-15;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLQLEHLLKLQMLNGINNY 32
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DB 1 APTSSSTKKTQLQLEHLLKLQMLNGINNY 31

RESULT 4
US-09-149-721-3
; Sequence 3, Application US/09149721
; Patent No. US20020058795A1
; GENERAL INFORMATION:
; APPLICANT: Mumper, Russ; Tagliaferri, Frank
; TITLE OF INVENTION: HYDROPHOBIC GLYCOSYLAMINE DERIVATIVES, COMPOSITIONS, AND METHODS
; FILE REFERENCE: 237/023
; CURRENT APPLICATION NUMBER: US/09/149,721
; CURRENT FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: 60/058,259
; PRIOR FILING DATE: 1997-09-08
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Microsoft Word
; SEQ ID NO 3
; LENGTH: 153
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of human IL-2
US-09-149-721-3

Query Match 93.0%; Score 147; DB 10; Length 153;
Best Local Similarity 96.8%; Pred. No. 4.1e-15;
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QY 2 APTSSSTKKTQLQLEHLLKLQMLNGINNY 32
|||||
DB 21 APTSSSTKKTQLQLEHLLKLQMLNGINNY 51

RESULT 5
US-09-923-246-111
; Sequence 111, Application US/09923246
; Patent No. US20020128446A1
; GENERAL INFORMATION:
; APPLICANT: No. US20020128446Alak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHALL LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/923,246
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217
; PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 111
; LENGTH: 153
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-923-246-111

Query Match 93.0%; Score 147; DB 10; Length 153;
Best Local Similarity 96.8%; Pred. No. 4.1e-15;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLQLEHLLKLQMLNGINNY 32
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DB 21 APTSSSTKKTQLQLEHLLKLQMLNGINNY 51

RESULT 6
US-09-766-543-14
; Sequence 14, Application US/09766543
; Patent No. US20020041865A1
; GENERAL INFORMATION:
; APPLICANT: Austin, Richard
; APPLICANT: Kwok, Cheuk S.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: METHODS FOR TREATING TUMORS
; FILE REFERENCE: PP01679.002
; CURRENT APPLICATION NUMBER: US/09/766,543
; CURRENT FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: 60/177,258
; PRIOR FILING DATE: 2000-01-20
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: hIL-2
US-09-766-543-14

; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: construct of human CD39
US-09-835-147-8

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Best Local Similarity 100.0%; Pred. No. 0.65;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQL 13
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Db 25 APTSSSTKKTQL 36

RESULT 11
US-09-835-147-26
; Sequence 26, Application US/09835147
; Patent No. US20020002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 487
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: construct of human CD39
US-09-835-147-26

Query Match 36.1%; Score 57; DB 10; Length 487;
Best Local Similarity 100.0%; Pred. No. 0.66;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 25 APTSSSTKKTQL 36

RESULT 12
US-09-881-752A-280
; Sequence 280, Application US/09881752A
; Patent No. US20020115078A1
; GENERAL INFORMATION:
; APPLICANT: Kleenhouse, Harold
; APPLICANT: Al-Garawi, Amal
; APPLICANT: Miller, Charles
; APPLICANT: Tomb, Jean-Francois
; APPLICANT: Comen, Raymond P.
; TITLE OF INVENTION: Identification of Polynucleotides

; TITLE OF INVENTION: Encoding No. US20020115078A1 Helicobacter Polypeptides in t
; TITLE OF INVENTION: Genome
; FILE REFERENCE: 06132/041002
; CURRENT APPLICATION NUMBER: US/09/881,752A
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 08/833,457
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 370
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 280
; LENGTH: 751
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-881-752A-280

Query Match 32.3%; Score 51; DB 10; Length 751;
Best Local Similarity 42.9%; Pred. No. 9;
Matches 12; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 5 SSSTKKTQLQLHLLKLQMLNGINNY 32
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Db 509 SESQKKDFIKLFGKILKLENILNSFNF 536

RESULT 13
US-09-815-242-11373
; Sequence 11373, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11373
; LENGTH: 866
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-815-242-11373

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Best Local Similarity 42.9%; Pred. No. 11;
Matches 12; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 5 SSSTKKTQLQLHLLKLQMLNGINNY 32
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RESULT 14
US-10-142-120-1
; Sequence 1, Application US/10142120
; Patent No. US20020164302A1
; GENERAL INFORMATION:
; APPLICANT: Epstein, Alan L.
; TITLE OF INVENTION: VASOPRESSIN-RECEPTOR ENHANCING PEPTIDE FRAGMENT OF HUMAN INTERLEUKIN-
; FILE REFERENCE: 1920-325D2-09801297
; CURRENT APPLICATION NUMBER: US/10/142,120
; CURRENT FILING DATE: 2002-05-09
; PRIOR APPLICATION NUMBER: 09/443,061
; PRIOR FILING DATE: 1999-11-18
; PRIOR APPLICATION NUMBER: 08/806,121
; PRIOR FILING DATE: 1996-12-23
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-142-120-1

Query Match 31.6%; Score 50; DB 9; Length 37;
Best Local Similarity 90.0%; Pred. No. 0.33;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 23 QMILNGINNY 32
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Db 1 EMILNGINNY 10

RESULT 15
US-09-796-149-5
; Sequence 5, Application US/09796149
; Patent No. US20020035079A1
; GENERAL INFORMATION:
; APPLICANT: Univ. of Southern California
; TITLE OF INVENTION: Mutated cyclin G1 protein
; FILE REFERENCE: 4-31342A/USC
; CURRENT APPLICATION NUMBER: US/09/796,149
; CURRENT FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-796-149-5

Query Match 29.7%; Score 47; DB 10; Length 226;
Best Local Similarity 60.0%; Pred. No. 8.4;
Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 8 TKKTQLQLEHLLKL 22
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Db 82 TKKQVLRMEHLVLKV 96

Search completed: February 20, 2003, 10:08:32
Job time : 8.12698 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 20, 2003, 10:00:37 ; Search time 30.0159 Seconds
(without alignments)
137.619 Million cell updates/sec

Title: US-09-776-781-8
Perfect score: 153
Sequence: 1 APTSSSKTKQLQLEHLLKLLQMLGINNY 31

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Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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23: /SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	153	100.0	31	23 ABB79535	Interleukin-2 pept
2	153	100.0	32	23 ABB79534	Interleukin-2 pept
3	153	100.0	133	21 AAY53825	Amino acid sequenc
4	150	98.0	133	21 AAY53829	Amino acid sequenc
5	149	97.4	133	21 AAY53828	Amino acid sequenc
6	149	97.4	134	8 AAP70573	Sequence of segmen
7	148	96.7	133	21 AAY53830	Amino acid sequenc
8	148	96.7	133	21 AAY53901	Amino acid sequenc
9	147	96.1	58	12 AAR11015	Human interleukin-
10	147	96.1	60	11 AAR06838	Human IL-2 N-termi

11	147	96.1	60	15 AAR48245	Human Interleukin-
12	147	96.1	88	17 AAR95433	Interleukin-2 ALPH
13	147	96.1	96	15 AAR68899	Human pro-insulin
14	147	96.1	96	16 AAP78662	Fusion protein con
15	147	96.1	120	6 AAP50864	Sequence of interl
16	147	96.1	128	12 AAR10906	Interleukin-2 muta
17	147	96.1	129	12 AAR10905	Interleukin-2 muta
18	147	96.1	129	12 AAR10908	Interleukin-2 muta
19	147	96.1	130	12 AAR10907	Interleukin-2 muta
20	147	96.1	131	4 AAP30044	Sequence of interl
21	147	96.1	131	6 AAP50217	Sequence of human
22	147	96.1	132	12 AAR10901	Interleukin-2 muta
23	147	96.1	132	12 AAR10902	Interleukin-2 muta
24	147	96.1	132	12 AAR10903	Interleukin-2 muta
25	147	96.1	132	12 AAR10904	Interleukin-2 muta
26	147	96.1	132	23 ABB79536	Human interleukin-
27	147	96.1	133	5 AAP40048	Sequence of an int
28	147	96.1	133	5 AAP40044	Sequence of mature
29	147	96.1	133	6 AAP50163	Sequence of the hu
30	147	96.1	133	6 AAP50857	Sequence of interl
31	147	96.1	133	6 AAP50858	Sequence of interl
32	147	96.1	133	6 AAP50859	Sequence of interl
33	147	96.1	133	6 AAP50860	Sequence of interl
34	147	96.1	133	6 AAP50861	Sequence of interl
35	147	96.1	133	6 AAP50862	Sequence of interl
36	147	96.1	133	6 AAP50863	Sequence of interl
37	147	96.1	133	7 AAP60833	Oxidation resistan
38	147	96.1	133	7 AAP60834	Oxidation resistan
39	147	96.1	133	7 AAP60835	Oxidation resistan
40	147	96.1	133	7 AAP60836	Oxidation resistan
41	147	96.1	133	7 AAP60837	Oxidation resistan
42	147	96.1	133	7 AAP60838	Oxidation resistan
43	147	96.1	133	7 AAP61100	Sequence of interl
44	147	96.1	133	7 AAP61651	Antigenic fragment
45	147	96.1	133	7 AAP61725	Plasmid pILOx135-8

ALIGNMENTS

RESULT 1
ABB79535
ID ABB79535 standard; Peptide; 31 AA.
AC ABB79535;
DT 23-SEP-2002 (first entry)
DE Interleukin-2 peptide IP131 (D20K).
KW IP131; interleukin-2; human; gene; gene therapy; mutant; mutein.
XX Homo sapiens.
OS Synthetic.
FH Key Location/Qualifiers
FT Misc-difference 20 /note= "wild-type Asp substituted by Lys"
XX US2002044935-A1.
XX 18-APR-2002.
XX 06-FEB-2001; 2001US-0776781.
XX 16-JUL-1998; 98US-0116594.
XX 12-SEP-2000; 2000US-0660465.
XX (INSP) INST PASTEUR.
XX Thereze J, Eckenberg R, Moreau J, Goldberg M, Rose T, Alzari P;
XX Mazie J;


```

FH Key Location/Qualifiers
FT Misc-difference 20 /note= "wild type Asp has been replaced with Lys"
PN WO9960128-A1.
XX 25-NOV-1999.
XX 13-MAY-1999; 99WO-US10643.
XX 15-MAY-1998; 98US-0080080.
XX (FARB ) BAYER CORP.
XX Shanafelt AB, Greve JM, Jesmok G, Lembach KJ, Wetzel GD;
XX WPI; 2000-086598/07.
XX New polypeptide comprising a human interleukin-2 (IL-2) mutein useful
XX for treating diseases such as HIV and cancer -
XX Example 5; Page -: 80pp; English.
XX AAY53822-66 represent human interleukin-2 (IL-2) muteins, where human
XX IL-2 has been substituted at one of positions 20, 88 or 126. Wild-type
XX IL-2, when used in cancer treatment, has adverse side effects. The
XX toxicities associated with IL-2 therapy include severe fever, nausea,
XX vomiting, vascular leak and serious hypotension. The muteins described
XX in this invention have reduced toxicity and are better tolerated. It is
XX the mediation of IL-2 through natural killer cells which causes the
XX toxicity whereas the efficacy is mediated by the direct activation of T
XX cells. The muteins preferentially activate T cells over natural killer
XX cells. IL-2 muteins may be used for treating a mammal afflicted with an
XX IL-2 treatable condition. The condition may be one of the following:
XX HIV, cancer including renal carcinoma and malignant melanoma, autoimmune
XX disease, infectious disease, immune deficiency including SCID or other
XX therapeutic application requiring general stimulation of the immune
XX system. Other potential uses include treatment of infectious diseases
XX such as tuberculosis and as an adjuvant in cancer vaccine strategy. The
XX DNA sequences encoding the IL-2 mutein may be used in gene therapy
XX applications in those diseases in which IL-2 is expected to provide an
XX effective therapy due to its T cell activity.
XX note: this sequence does not appear in the specification; it was created
XX using information provided and the wild type IL-2 sequence (see
XX AAY53821).
SQ Sequence 133 AA;
Query Match 100.0%; Score 153; DB 21; Length 133;
Best Local Similarity 100.0%; Pred. No. 5.8e-14;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APTSSSTKKTQLQLHLLKLQMLNGINNY 31
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Db 1 APTSSSTKKTQLQLHLLKLQMLNGINNY 31
| | | | | | | | | | | | | | | | | | | | |
RESULT 4
AAY53829
ID AAY53829 standard; Protein; 133 AA.
XX
AC AAY53829;
XX
DT 13-MAR-2000 (first entry)
XX
DE Amino acid sequence of human interleukin-2 (IL-2) mutein D20R.
XX
KW Human; interleukin-2; IL-2; IL-2 mutein; HIV; cancer; renal carcinoma;
KW malignant melanoma; autoimmune disease; infectious disease;
KW immune deficiency; SCID; tuberculosis; adjuvant; cancer vaccine;
KW gene therapy.
XX
OS Synthetic.

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```

OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 20 /note= "wild type Asp has been replaced with Arg"
PN WO9960128-A1.
XX 25-NOV-1999.
XX 13-MAY-1999; 99WO-US10643.
XX 15-MAY-1998; 98US-0080080.
XX (FARB ) BAYER CORP.
XX Shanafelt AB, Greve JM, Jesmok G, Lembach KJ, Wetzel GD;
XX WPI; 2000-086598/07.
XX New polypeptide comprising a human interleukin-2 (IL-2) mutein useful
XX for treating diseases such as HIV and cancer -
XX Example 5; Page -: 80pp; English.
XX AAY53822-66 represent human interleukin-2 (IL-2) muteins, where human
XX IL-2 has been substituted at one of positions 20, 88 or 126. Wild-type
XX IL-2, when used in cancer treatment, has adverse side effects. The
XX toxicities associated with IL-2 therapy include severe fever, nausea,
XX vomiting, vascular leak and serious hypotension. The muteins described
XX in this invention have reduced toxicity and are better tolerated. It is
XX the mediation of IL-2 through natural killer cells which causes the
XX toxicity whereas the efficacy is mediated by the direct activation of T
XX cells. The muteins preferentially activate T cells over natural killer
XX cells. IL-2 muteins may be used for treating a mammal afflicted with an
XX IL-2 treatable condition. The condition may be one of the following:
XX HIV, cancer including renal carcinoma and malignant melanoma, autoimmune
XX disease, infectious disease, immune deficiency including SCID or other
XX therapeutic application requiring general stimulation of the immune
XX system. Other potential uses include treatment of infectious diseases
XX such as tuberculosis and as an adjuvant in cancer vaccine strategy. The
XX DNA sequences encoding the IL-2 mutein may be used in gene therapy
XX applications in those diseases in which IL-2 is expected to provide an
XX effective therapy due to its T cell activity.
XX note: this sequence does not appear in the specification; it was created
XX using information provided and the wild type IL-2 sequence (see
XX AAY53821).
SQ Sequence 133 AA;
Query Match 98.0%; Score 150; DB 21; Length 133;
Best Local Similarity 96.8%; Pred. No. 1.5e-13;
Matches 30; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 APTSSSTKKTQLQLHLLKLQMLNGINNY 31
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Db 1 APTSSSTKKTQLQLHLLKLQMLNGINNY 31
| | | | | | | | | | | | | | | | | | | | |
RESULT 5
AAY53828
ID AAY53828 standard; Protein; 133 AA.
XX
AC AAY53828;
XX
DT 13-MAR-2000 (first entry)
XX
DE Amino acid sequence of human interleukin-2 (IL-2) mutein D20Q.
XX
KW Human; interleukin-2; IL-2; IL-2 mutein; HIV; cancer; renal carcinoma;
KW malignant melanoma; autoimmune disease; infectious disease;
KW immune deficiency; SCID; tuberculosis; adjuvant; cancer vaccine;
KW gene therapy.
XX
OS

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[illegible]

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PI Shanafelt AB, Greve JM, Jesmok G, Lembach KJ, Wetzel GD;
XX WPI; 2000-086598/07.
XX
XX New polypeptide comprising a human interleukin-2 (IL-2) mutein useful
XX for treating diseases such as HIV and cancer
XX
XX Example 5; Page -: 80pp; English.
XX
XX AAY53822-66 represent human interleukin-2 (IL-2) muteins, where human
XX IL-2 has been substituted at one of positions 20, 88 or 126. Wild-type
XX IL-2, when used in cancer treatment, has adverse side effects. The
XX toxicities associated with IL-2 therapy include severe fever, nausea,
XX vomiting, vascular leak and serious hypotension. The muteins described
XX in this invention have reduced toxicity and are better tolerated. It is
XX the mediation of IL-2 through natural killer cells which causes the
XX toxicity whereas the efficacy is mediated by the direct activation of T
XX cells. The muteins preferentially activate T cells over natural killer
XX cells. IL-2 muteins may be used for treating a mammal afflicted with an
XX IL-2 treatable condition. The condition may be one of the following:
XX HIV, cancer including renal carcinoma and malignant melanoma, autoimmune
XX disease, infectious disease, immune deficiency including SCID or other
XX therapeutic application requiring general stimulation of the immune
XX system. Other potential uses include treatment of infectious diseases
XX such as tuberculosis and as an adjuvant in cancer vaccine strategy. The
XX DNA sequences encoding the IL-2 mutein may be used in gene therapy
XX applications in those diseases in which IL-2 is expected to provide an
XX effective therapy due to its T cell activity.
XX note: this sequence does not appear in the specification; it was created
XX using information provided and the wild type IL-2 sequence (see
XX AAY53821).
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XX Sequence 133 AA;
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XX DB 1 APTSSSTKKTQLQLEHLLKLQMLINGINNY 31
XX |||||
XX
XX RESULT 8
XX AAY53901
XX ID AAY53901 standard; Protein; 133 AA.
XX AC AAY53901;
XX DT 13-MAR-2000 (first entry)
XX
XX DE Amino acid sequence of human interleukin-2 (IL-2) mutein D20N.
XX
XX KW Human; interleukin-2; IL-2; IL-2 mutein; HIV; cancer; renal carcinoma;
XX malignant melanoma; autoimmune disease; infectious disease;
XX KW immune deficiency; SCID; tuberculosis; adjuvant; cancer vaccine;
XX KW gene therapy.
XX
XX OS Synthetic.
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
XX FT Misc-difference 20
XX FT /note= "wild type Asp has been replaced with Asn"
XX
XX PN WO9560128-A1.
XX PD 25-NOV-1999.
XX
XX PF 13-MAY-1999; 99WO-US10643.
XX
XX PR 15-MAY-1998; 98US-0080080.
XX

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PA (FARB ) BAYER CORP.
XX
XX Shanafelt AB, Greve JM, Jesmok G, Lembach KJ, Wetzel GD;
XX WPI; 2000-086598/07.
XX
XX New polypeptide comprising a human interleukin-2 (IL-2) mutein useful
XX for treating diseases such as HIV and cancer
XX
XX Example 5; Page -: 80pp; English.
XX
XX The present sequence is a human interleukin-2 (IL-2) mutein, where human
XX IL-2 has been substituted at one of positions 20, 88 or 126. Wild-type
XX IL-2, when used in cancer treatment, has adverse side effects. The
XX toxicities associated with IL-2 therapy include severe fever, nausea,
XX vomiting, vascular leak and serious hypotension. The muteins described
XX in this invention have reduced toxicity and are better tolerated. It is
XX the mediation of IL-2 through natural killer cells which causes the
XX toxicity whereas the efficacy is mediated by the direct activation of T
XX cells. The muteins preferentially activate T cells over natural killer
XX cells. IL-2 muteins may be used for treating a mammal afflicted with an
XX IL-2 treatable condition. The condition may be one of the following:
XX HIV, cancer including renal carcinoma and malignant melanoma, autoimmune
XX disease, infectious disease, immune deficiency including SCID or other
XX therapeutic application requiring general stimulation of the immune
XX system. Other potential uses include treatment of infectious diseases
XX such as tuberculosis and as an adjuvant in cancer vaccine strategy. The
XX DNA sequences encoding the IL-2 mutein may be used in gene therapy
XX applications in those diseases in which IL-2 is expected to provide an
XX effective therapy due to its T cell activity.
XX note: this sequence does not appear in the specification; it was created
XX using information provided and the wild type IL-2 sequence (see
XX AAY53821).
XX
XX Sequence 133 AA;
XX
XX Query Match 96.7%; Score 148; DB 21; Length 133;
XX Best Local Similarity 96.8%; Pred. No. 3e-13;
XX Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 APTSSSTKKTQLQLEHLLKLQMLINGINNY 31
XX |||||
XX DB 1 APTSSSTKKTQLQLEHLLKLQMLINGINNY 31
XX |||||
XX
XX RESULT 9
XX AAR11015
XX ID AAR11015 standard; Peptide; 58 AA.
XX AC AAR11015;
XX DT 13-MAY-1991 (first entry)
XX
XX DE Human interleukin-2-derived stabiliser peptide.
XX
XX KW interleukin-2; IL-2; gag 24; gp 41; gp 36; HIV detection.
XX
XX OS Homo sapiens.
XX
XX PN EP416673-A.
XX
XX PD 13-MAR-1991.
XX
XX PF 02-AUG-1990; 90EP-0202108.
XX
XX PR 03-AUG-1989; 89CU-0000149.
XX
XX (INGE-) CENT ING GENETICA.
XX
XX Novoa Perez LI, Machado Lahera JA, Fernandez Maso JR;
XX Benitez Fuentes JV, Narciani Diaz RE, Rodriguez Reinoso JL;
XX Estrada Garcia MP, Garcia Suarez J, Herrera Martinez LS;
XX

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DR WPI; 1991-075192/11.
XX N-PSDB; AAQ10898.
PT Method for expressing heterologous proteins - as fusion protein,
PT using vector contg. stabilising sequence
XX
XX Claim 2; Page 10; 18pp; English.
XX
CC The sequence corresponds to the first 58 amino acid residues of
CC human IL-2. It forms part of a fusion protein, linked to a
CC heterologous protein. The heterologous protein is preferably gag 24
CC or a fragment of gp 41 of HIV-1 or it is a fragment of gp 36 of
CC HIV-2. Such fusion proteins can be used to detect antibodies to
CC these proteins. See also AAQ10899-Q10903.
XX
SQ Sequence 58 AA;

Query Match 96.1%; Score 147; DB 12; Length 58;
Best Local Similarity 96.8%; Pred. No. 1.7e-13;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 APTSSSTKKTQLEHLLKLQMLINGINNY 31
Db 2 APTSSSTKKTQLEHLLLDLQMLINGINNY 32

RESULT 10
AAR06838
ID AAR06838 standard; protein; 60 AA.
XX
AC AAR06838;
XX
XX 14-JAN-1991 (first entry)
XX
XX Human IL-2 N-terminal transcript of plasmid pTl3S.
XX
XX Bovine tuberculosis; Interleukin-2; IL-2; plasmid pTl3S.
XX
XX Mycobacterium bovis.
XX
XX JF02195895-A.
XX
XX 02-AUG-1990.
XX
XX 24-JAN-1989; 89JP-0013270.
XX
XX 24-JAN-1989; 89JP-0013270.
XX
XX (AJIN ) AJINOMOTO KK.
XX
XX WPI; 1990-278851/37.
XX
XX N-PSDB; AAQ05976.
XX
XX BCG bacteria derived immuno:protein MPB70 - can be used as
XX diagnostic agent used to determine bovine tuberculosis.
XX
XX Disclosure; Fig 2; 11pp; Japanese.
XX
XX Immunoprotein MPB 70 encoding sequence may be incorporated into
XX plasmid pTl3S with an N-terminal fragment of human IL-2. The plasmid
XX may be used to transform an expression system giving a fusion
XX protein which may be used as a diagnostic agent for bovine
XX tuberculosis infection.
XX
SQ Sequence 60 AA;

Query Match 96.1%; Score 147; DB 11; Length 60;
Best Local Similarity 96.8%; Pred. No. 1.7e-13;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 APTSSSTKKTQLEHLLKLQMLINGINNY 31
Db 2 APTSSSTKKTQLEHLLLDLQMLINGINNY 32

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RESULT 11
AAR48245
ID AAR48245 standard; Protein; 60 AA.
XX
XX AAR48245;
XX
XX 12-JUL-1994 (first entry)
XX
XX Human Interleukin-2.
XX
XX non-coding region; coding region; resonance; interaction; IL-2;
XX optimisation; degenerate sequence; plasmid pTl3SMco; pT9-11;
XX gene expression; regulation; recombinant protein production;
XX Interleukin-2; interleukin-6.
XX
XX Homo sapiens.
XX
XX FR2692594-A.
XX
XX 24-DEC-1993.
XX
XX 22-JUN-1992; 92FR-0007571.
XX
XX 22-JUN-1992; 92FR-0007571.
XX
XX (PERE/) PEREZ J.
XX
XX Perez J;
XX
XX WPI; 1994-028256/04.
XX
XX N-PSDB; AAQ55629, AAQ55630.
XX
XX Application of optimised gene expression - for scientific,
XX Industrial and therapeutic purposes
XX
XX Disclosure; Fig 28 and Fig 29; 110pp; French.
XX
XX Resonances between coding and non-coding regions were measured for
XX the native human IL-2 gene in plasmid pT911 (see AAQ55630) and a
XX synthetic IL-2 gene (AAQ55629) in which alternative, degenerate
XX codons were used in order to introduce additional restriction
XX sites. It was found that the degenerate changes greatly upset the
XX "natural order" between coding and non-coding regions; as a result,
XX the amount of protein expressed by the degenerate gene is likely to
XX be adversely affected. The inventors have proposed an "optimised"
XX IL-2 gene with the aim of increasing the amount of protein expressed
XX by the gene. (N.B. the sequence is also described as
XX Interleukin-6).
XX
SQ Sequence 60 AA;

Query Match 96.1%; Score 147; DB 15; Length 60;
Best Local Similarity 96.8%; Pred. No. 1.7e-13;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 APTSSSTKKTQLEHLLKLQMLINGINNY 31
Db 2 APTSSSTKKTQLEHLLLDLQMLINGINNY 32

```

```

RESULT 12
AAR95433
ID AAR95433 standard; Protein; 88 AA.
XX
XX AAR95433;
XX
XX 17-SEP-1996 (first entry)
XX
XX Interleukin-2 ALPHA segment.
XX
XX Multifunctional protein; targetted hetero-association;
XX

```

KW protein assembly; antibody engineering; interleukin-2; IL-2;
 KW cytokine; tumour; therapy.
 XX Synthetic.

PN WO9613583-A2.

XX 09-MAY-1996.

XX 20-OCT-1995; 95WO-EP04117.

XX 20-OCT-1994; 94EP-0116558.

XX (MORP-) MORPHOSYS GES PROTEINOPTIMIERUNG MBH.

XX Lupas A, Pack P;

XX WPI; 1996-239496/24.

XX N-PSDB; AAT15267.

XX Targetted hetero-association of recombinant proteins to
 PT multi-functional complexes - useful for therapeutic and diagnostic
 PT purposes

PS Example 3; Fig 13; 34pp; English.

CC Human interleukin-2 (IL-2) can be used as an assembly device for
 CC the targetted hetero-association of recombinant proteins. The IL-2
 CC is segmented between His79 and Lys80 to form ALPHA (AAR95433) and
 CC BETA (AAR95434) segments encoded by MroI-AscI-HindIII gene cassettes
 CC (AAT15267 and AAT15268, respectively). The device combines the low
 CC immunogenicity of the plasmatic protein with a preferable effector
 CC function of the native-like cytokine structure and an inter-
 CC segmental cysteine bridge (Cys58-Cys105) after assembly. The
 CC combination of 1 or more antibody fragments against tumour antigens
 CC with additional cytokines, e.g. IL-6 or IL-12, targets the
 CC multi-cytokine complex directly to the tumour.

XX Sequence 88 AA;

Query Match 96.1%; Score 147; DB 17; Length 88;
 Best Local Similarity 96.8%; Pred. No. 2.6e-13;
 Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 APTSSSTKKTQLQLEHLLKQMLNGINNY 31

Db 3 APTSSSTKKTQLQLEHLLKQMLNGINNY 33

RESULT 13

AAR68899
 ID AAR68899 standard; peptide; 96 AA.

XX AAR68899;

DT 02-MAR-1995 (first entry)

DE Human pro-insulin 2.

XX Pro-insulin; A-chain; B-chain; C-chain; disulphide;
 KW mercaptan; chaotropic agent.

XX Homo sapiens.

XX EP600372-A.

XX 08-JUN-1994.

XX 25-NOV-1993; 93EP-0118993.

XX 02-DEC-1992; 92DE-4240420.

XX (FARH) HOECHST AG.

XX Gerl M, Ludwig J, Obermeier R, Sabel W;
 PI WPI; 1994-177718/22.
 XX Prodn. of pro-insulin with correct di: sulphide bridges - by
 PT treating recombinant precursor protein with mercaptan in alkali
 PT and in presence of chaotropic agent, then isolation on
 PT hydrophobic resin
 XX Disclosure; Page 11; 15pp; German.
 PS Pro-insulin is produced by treating recombinant precursor protein
 CC with a mercaptan to provide 2-10 SH residues per Cys residue, in
 CC presence of a chaotropic agent and in aq. medium of pH 10-11,
 CC treating the prod. with 3-50 g hydrophobic adsorber resin per 1 aq.
 CC medium of pH 4-7, isolating the adsorbed resin and pro-insulin and
 CC desorbing the pro-insulin. This method produces pro-insulin with
 CC correctly bonded Cys bridges. Compared with known methods it
 CC involves fewer stages (esp. no sulphitolyis or cyanogen bromide
 CC cleavage) and overall losses during purification are reduced, i.e.
 CC the process is quicker and gives better yields.
 CC Sequences of insulin chain A, B and C are given in AAR68895-97.
 CC Sequences of pro-insulin 1-4 are given in AAR68898-901.

XX Sequence 96 AA;

Query Match 96.1%; Score 147; DB 15; Length 96;
 Best Local Similarity 96.8%; Pred. No. 2.9e-13;
 Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 APTSSSTKKTQLQLEHLLKQMLNGINNY 31

Db 2 APTSSSTKKTQLQLEHLLKQMLNGINNY 32

RESULT 14

AAR78662
 ID AAR78662 standard; protein; 96 AA.

XX AAR78662;

DT 03-APR-1996 (first entry)

XX Fusion protein contg. proinsulin sequence 3.

XX Proinsulin; post-translational modification; recombinant production;
 KW protein folding; conformation.

XX Synthetic.

XX Key Location/Qualifiers

FT Region 41..44

FT /label= R2

FT /note= "a peptide of 4 amino acids"

FT Peptide 45..74

FT /label= R1-(B2-B29)-Y

FT /note= "human insulin B-chain"

FT Region 75

FT /label= X

FT Peptide 76..96

FT /label= Gly-(A2-A20)-R3

FT /note= "human insulin A-chain"

XX EP668292-A2.

XX 23-AUG-1995.

XX 09-FEB-1995; 95EP-0101748.

XX 18-FEB-1994; 94DE-4405179.

XX (FARH) HOECHST AG.

XX Gerl M, Ludwig J, Obermeier R, Sabel W;
 XX WPI; 1995-284754/38.
 XX Isolation of insulin that is correctly post-translationally
 PT processed - by reacting pro:insulin with a mercaptan in the presence
 PT of a chaotropic agent and purificn. after absorption to hydrophobic
 PT resin
 XX
 XX Example 2; Page 8; 16pp; German.
 XX
 CC The present sequence is that of a fusion protein, produced in E.coli
 CC which contains an example of a proinsulin molecule corresp.
 CC to the general formula R2-R1-(B2-B29)-Y-X-Gly-(A2-A20)-R3 (II). In
 CC formula (II), X = Lys, Arg or a peptide of 2-35 amino acids contg.
 CC Lys or Arg at the N- and C-termini; Y = a natural amino acid; R1 =
 CC Phe or a bond; R2 = H, Arg, Lys, a peptide of 2-45 amino acids
 CC contg. Arg or Lys at the N- and C-termini; R3 = a natural amino
 CC acid; (A2-A20) and (B2-B29) are the insulin A- and B-chain sequences
 CC from human or other insulin. The proinsulin molecule, released by
 CC cyanogen bromide, is reacted with mercaptan at a ratio of 2-10 SH
 CC residues of mercaptan per Cys residue of proinsulin. The reaction
 CC takes place in the presence of a chaotropic auxiliary agent at
 CC pH 10-11 and results in proinsulin with correctly linked cystine
 CC bridges. Reaction with trypsin and opt. carboxypeptidase B yields
 CC correctly folded insulin. The insulin is isolated by absorption on
 CC a hydrophobic resin.
 XX

SQ Sequence 96 AA;

Query Match 96.1%; Score 147; DB 16; Length 96;
 Best Local Similarity 96.8%; Pred. No. 2.9e-13;
 Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 APTSSSTKKTQLEHLLKLQMLINGINNY 31
 |||||
 DB 2 APTSSSTKKTQLEHLLKLQMLINGINNY 32

RESULT 15

AAP50864
 ID AAP50864 standard; Protein; 120 AA.

XX AAP50864;

XX 03-OCT-2002 (updated)

DT 01-DEC-1991 (first entry)

XX Sequence of interleukin II (IL-2) analogue 341 [Stop121] IL-II.

DE Immunotherapy; lymphokine; interleukin-2; thymocyte mitogenesis.

XX Synthetic.

XX WO8500817-A.

XX 28-FEB-1985.

XX 09-AUG-1984; 84WO-US01252.

XX 03-AUG-1984; 84US-0635941.

PR 10-AUG-1983; 83US-0521967.

XX (AMGE-) AMGEN.

XX Souza LM, Stabinsky Y;

XX WPI; 1985-062280/10.

XX Microbial expression of interleukin II and analogues - by using

PT manufactured DNA sequences to transform microorganisms

XX

PS Claim 341; Page 35; 39pp; English.
 XX
 CC The inventors claim a manufactured gene for the prodn. of IL-2 and
 CC analogues, and for polypeptides of IL-2 and analogues, and for
 CC methods for their recombinant production.
 CC (Updated on 03-OCT-2002 to add missing OS field.)
 XX

SQ Sequence 120 AA;

Query Match 96.1%; Score 147; DB 6; Length 120;
 Best Local Similarity 96.8%; Pred. No. 3.7e-13;
 Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 APTSSSTKKTQLEHLLKLQMLINGINNY 31
 |||||

DB 1 APTSSSTKKTQLEHLLKLQMLINGINNY 31
 |||||

Search completed: February 20, 2003, 10:05:04
 Job time : 31.0159 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 20, 2003, 10:03:27 ; Search time 28.0476 Seconds
(without alignments)
106.254 Million cell updates/sec

Title: US-09-776-781-8
Perfect score: 153
Sequence: 1 APTSSSTKTKQLQLEHLLKQLMILNINNY 31

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR73:*
1: pirl.*
2: pirl2.*
3: pirl3.*
4: pirl4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match	Length	DB ID	Description
1	147	96.1	153	1	ICHU2
2	147	96.1	153	1	ICG12
3	107	69.9	154	2	JN0698
4	97	63.4	155	2	A31278
5	96	62.7	154	2	S16241
6	95	62.1	155	2	S33509
7	85	55.6	149	2	S31391
8	72	47.1	155	2	S38662
9	72	47.1	155	2	S11488
10	72	47.1	155	2	I45913
11	69	45.1	169	2	S37289
12	64	41.8	169	1	ICMS2
13	61	39.9	189	2	H64307
14	54	35.3	1061	1	GNLJG4
15	53	34.6	357	2	S12169
16	53	34.6	452	2	B84483
17	52.5	34.3	60	2	I68870
18	51.5	33.7	62	2	I54512
19	51.5	33.7	415	2	I51637
20	51	33.3	737	2	G82262
21	51	33.3	866	2	F64625
22	51	33.3	875	2	B71890
23	50.5	33.0	72	2	I68871
24	50.5	33.0	741	2	A45771
25	50	32.7	304	2	F95285
26	50	32.7	543	2	F62217
27	49.5	32.4	367	2	E84453
28	49.5	32.4	474	2	S31712
29	49	32.0	145	2	HB3921

30	48.5	31.7	452	2	G54679
31	48	31.4	398	2	B70209
32	48	31.4	441	2	AB1367
33	48	31.4	441	2	AC1736
34	48	31.4	765	2	S76795
35	48	31.4	1964	2	A59282
36	47.5	31.0	127	1	NR80K2
37	47.5	31.0	244	2	T11685
38	47.5	31.0	288	2	B99930
39	47	30.7	257	2	S39521
40	47	30.7	307	2	T46103
41	47	30.7	406	2	S24788
42	47	30.7	432	2	S08277
43	47	30.7	511	2	D71687
44	47	30.7	564	2	S76672
45	47	30.7	943	2	S44636

ALIGNMENTS

RESULT 1

ICHU2
Interleukin-2 precursor [validated] - human
A:Alternate names: IL-2; T-cell growth factor
C:Species: Homo sapiens (man)
C:Date: 11-Aug-1983 #sequence_revision 11-Aug-1983 #text_change 08-Dec-2000
C:Accession: A01849; A21192; A20961; S31209; A93297; A90113; A93478; I56518; I73624;
R:Holbrook, N.J.; Lieber, M.; Crabtree, G.R.
Nucleic Acids Res. 12, 5005-5013, 1984
A>Title: DNA sequence of the 5' flanking region of the human interleukin 2 gene: homo
A:Reference number: A93524; MUID:84247353; PMID:6330695
A:Accession: A01849
A:Molecule type: DNA
A:Residues: 1-153 <HO2>
A:Cross-references: GB:X00695; GB:X00200; GB:X00201; GB:X00202; NID:933783; PIDN:CAA2
R:Fujita, T.; Takaoka, C.; Matsui, H.; Taniguchi, T.
Proc. Natl. Acad. Sci. U.S.A. 80, 7437-7441, 1983
A>Title: Structure of the human interleukin 2 gene.
A:Reference number: A21192; MUID:84170243; PMID:6324170
A:Accession: A21192
A:Molecule type: DNA
A:Residues: 1-153 <FU>
A:Cross-references: GB:J00264; NID:9186294; PIDN:AAD48509.1; PID:9579676
R:Holbrook, N.J.; Smith, K.A.; Fornace Jr., A.J.; Comeau, C.M.; Wiskocil, R.L.; Crabt
Proc. Natl. Acad. Sci. U.S.A. 81, 1634-1638, 1984
A>Title: T-cell growth factor: complete nucleotide sequence and organization of the g
A:Reference number: A20961; MUID:84170356; PMID:6608729
A:Accession: A20961
A:Molecule type: DNA
A:Residues: 1-153 <HO2>
A:Cross-references: GB:K02056; NID:9186302; PIDN:AAA98792.1; PID:9386819
R:Laabi, Y.; Gras, M.P.; Carbonnel, F.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Tsapi
EMBO J. 11, 3897-3904, 1992
A>Title: A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene by a t(
A:Reference number: S31208; MUID:93010984; PMID:1396583
A:Accession: S31209
A:Molecule type: mRNA
A:Residues: 11-117 <LAA>
A:Cross-references: EMBL:Z14955
A>Note: this sequence is shown from the beginning of the fragment to the chromosomal
R:Taniguchi, T.; Matsui, H.; Fujita, T.; Takaoka, C.; Kashima, N.; Yoshimoto, R.; Ham
Nature 302, 305-310, 1983
A>Title: Structure and expression of a cloned cDNA for human interleukin-2.
A:Reference number: A93297; MUID:83167472; PMID:6403867
A:Accession: A93297
A:Molecule type: mRNA
A:Residues: 1-153 <TAN>
A:Cross-references: GB:V00564; NID:933780; PIDN:CAA23827.1; PID:933781
A:Experimental source: leukemic T-cell line, Jurkat-111, Cloned from Jurkat-FHCRC
R:Maeda, S.; Nishino, N.; Obaru, K.; Mita, S.; Nomiya, H.; Shimada, K.; Fujimoto, K
Biochem. Biophys. Res. Commun. 115, 1040-1047, 1983
A>Title: Cloning of interleukin 2 mRNAs from human tonsils.

A:Reference number: A90113; MUID:84023840; PMID:6312994
A:Accession: A90113
A:Molecule type: mRNA
A:Residues: 1-153 <NAE>
A:Cross-references: GB:J00264; NID:g186294; PIDN:AA48509.1; PID:g5729676
A:Experimental source: tonsillar mononuclear cells
R:Devos, R.; Platinck, G.; Cheroutre, H.; Simons, G.; Degraeve, W.; Tavernier, J.; Remau
Nucleic Acids Res. 11, 4307-4323, 1983
A:Title: Molecular cloning of human interleukin 2 cDNA and its expression in Escherichia
A:Reference number: A93478; MUID:83246551; PMID:6306584
A:Accession: A93478
A:Molecule type: mRNA
A:Residues: 1-153 <DEV>
A:Cross-references: GB:Y00564; NID:g33780; PIDN:CAA23827.1; PID:g33781
A:Experimental source: splenocytes
R:Eizenberg, O.; Faber-Elman, A.; Lotan, M.; Schwartz, M.
J. Neurochem. 64, 1928-1936, 1995
A:Title: Interleukin-2 transcripts in human and rodent brains: possible expression by as
A:Reference number: I56518; MUID:95239150; PMID:7722480
A:Accession: I56518
A:Molecule type: mRNA
A:Status: translated from GB/EMBL/DDBJ
A:Residues: 1-152 <ETZ>
A:Cross-references: GB:S77834; NID:g999000
A:Accession: I73624
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 5-7, 'F', '9-17', 'P', '19-32', 'X', '34-45', 'X', '47-143 <RES>
A:Cross-references: GB:S77835; NID:g999001; PIDN:AA4264.1; PID:g4261964
R:Nishino, N.; Obaru, K.; Maeda, S.; Shmada, K.; Onoue, K.
Biomed. Res. 6, 197-205, 1985
A:Title: Organization of the DNA regions flanking the human interleukin 2 gene.
A:Reference number: I52528
A:Accession: I52528
A:Status: translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-68 <RE3>
A:Cross-references: GB:M33199; NID:g186296; PIDN:AAA59139.1; PID:g553508
R:Stebenlist, U.; Durand, D.B.; Bressler, P.; Holbrook, N.J.; Norris, C.A.; Kamoun, M.;
Mol. Cell. Biol. 6, 3042-3049, 1986
A:Title: Promoter region of interleukin-2 gene undergoes chromatin structure changes and
A:Reference number: I57603; MUID:87084618; PMID:3491296
A:Accession: I57603
A:Status: translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-68 <RE3>
A:Cross-references: GB:M13879; NID:g186305; PIDN:AAA59141.1; PID:g553509
R:Weir, M.P.; Chaplin, M.A.; Wallace, D.M.; Dykes, C.W.; Hobden, A.N.
Biochemistry 27, 6883-6892, 1988
A:Title: Structure-activity relationships of recombinant human interleukin 2.
A:Reference number: I52401; MUID:89062420; PMID:3264184
A:Contents: recombinant IL-2 and mutants expressed in E. coli
A:Accession: I52401
A:Status: translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 'M', '21-153 <REA>
A:Cross-references: GB:M22005; NID:g186300; PIDN:AAA59140.1; PID:g386818
A:Note: mutation of Phe-42 to Ala reduced binding to the IL-2 receptor 5-10 fold without
R:Robb, R.J.; Kutny, R.M.; Panico, M.; Morris, H.R.; Chowdhry, V.
Proc. Natl. Acad. Sci. U.S.A. 81, 6486-6490, 1984
A:Title: Amino acid sequence and post-translational modification of human interleukin 2.
A:Reference number: A94009; MUID:85038540; PMID:6333684
A:Accession: A94009
A:Molecule type: protein
A:Residues: 21-153 <ROB>
A:Note: disulfide bonds and carbohydrate binding site were determined
A:Note: heterogeneity in Jurkat-derived IL-2 is primarily due to differences in glycosyl
n in lacking 21-Ala (FT-IL2-A and FT-IL2-B) and 22-Pro (FT-IL2-B)
R:Conradt, H.S.; Nimtz, M.; Dittmar, K.E.J.; Lindenmaier, W.; Hoppe, J.; Hauser, H.
J. Biol. Chem. 264, 17368-17373, 1989
A:Title: Expression of human interleukin-2 in recombinant baby hamster kidney, Ltk-, and
de.
A:Reference number: A34463; MUID:90008901; PMID:2793860

A:Accession: A34463
A:Molecule type: protein
A:Residues: 21-35 <CON>
A:Note: the O-linked glycosylation site in recombinant material matched that from hum
R:Grabenhorst, E.; Hofer, B.; Nimtz, M.; Jaeger, V.; Conradt, H.S.
Eur. J. Biochem. 215, 189-197, 1993
A:Title: Biosynthesis and secretion of human interleukin 2 glycoproteins variants fro
A:Reference number: S34052; MUID:93345493; PMID:8344280
A:Contents: annotation; glycosylation of variant forms expressed in insect cells
C:Genetics:
A:Gene: GDB:IL2
A:Cross-references: GDB:119344; OMIM:147680
A:Map position: 4q26-4q27
A:Introns: 49/3; 69/3; 117/3
C:Superfamily: Interleukin-2
C:Keywords: cytokine; glycoprotein; growth factor; immunoregulation; lymphokine; T-ce
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-153/Product: interleukin-2 #status experimental <IL2>
F:23/Binding site: carbohydrate (Thr) (covalent) #status experimental
F:78-125/Disulfide bonds: #status experimental
Query Match 96.1%; Score 147; DB 1; Length 153;
Best Local Similarity 96.8%; Pred. No. 5.6e-14;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 APTSSSTKTKTQLQLEHLLKLQMLINGINNY 31
|||||
DB 21 APTSSSTKTKTQLQLEHLLKLQMLINGINNY 51
|||||
RESULT 2
ICG12
Interleukin-2 precursor - common gibbon
N:Alternate names: IL-2; T-cell growth factor
C:Species: Hylobates lar (Common gibbon, white-handed gibbon)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 22-Jun-1999
C:Accession: A94067; A01849
R:Chen, S.J.; Holbrook, N.J.; Mitchell, K.F.; Vallone, C.A.; Greengard, J.S.; Crabtre
Proc. Natl. Acad. Sci. U.S.A. 82, 7284-7288, 1985
A:Title: A viral long terminal repeat in the interleukin 2 gene of a cell line that c
A:Reference number: A94067; MUID:86042650; PMID:3877307
A:Accession: A94067
A:Molecule type: mRNA
A:Residues: 1-153 <CHE>
A:Cross-references: GB:M11144; NID:g177014; PIDN:AAA35454.1; PID:g177015
A:Experimental source: leukemia cell line M1A 144; ATCC TIB 201
A:Note: the integration of a retrovirus sequence containing a 5' LTR into the 3' nonc
C:Superfamily: Interleukin-2
C:Keywords: cytokine; glycoprotein; growth factor; immunoregulation; lymphokine; T-ce
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-153/Product: interleukin-2 #status predicted <IL2>
F:23/Binding site: carbohydrate (Thr) (covalent) #status predicted
F:78-125/Disulfide bonds: #status predicted
Query Match 96.1%; Score 147; DB 1; Length 153;
Best Local Similarity 96.8%; Pred. No. 5.6e-14;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 APTSSSTKTKTQLQLEHLLKLQMLINGINNY 31
|||||
DB 21 APTSSSTKTKTQLQLEHLLKLQMLINGINNY 51
|||||
RESULT 3
JN0698
Interleukin 2 precursor - cat
C:Species: Felis silvestris catus (domestic cat)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 16-Jul-1999
C:Accession: JN0698
R:Cozzi, P.J.; Padrid, P.A.; Takeda, J.; Alegre, M.L.; Yuhki, N.; Leff, A.R.
Biochem. Biophys. Res. Commun. 194, 1038-1043, 1993
A:Title: Sequence and functional characterization of feline interleukin 2.
A:Reference number: JN0698; MUID:93356765; PMID:8352761

A:Accession: JN0698
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-154 <GO>
A:Cross-references: GB:L19402; NID:g304313; PIDN:AAA02865.1; PID:g304314
C:Superfamily: interleukin-2
C:Keywords: growth factor

Query Match
Best Local Similarity 69.9%; Score 107; DB 2; Length 154;
Matches 21; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 APTSSSTKKTQLEHLLKQLMILNGINN 30
DB 21 APASSSTKKTQLEHLLKQLMILNGINN 50

RESULT 4
A31278
interleukin-2 precursor - rat
N:Alternate names: IL-2; T-cell growth factor
C:Species: Rattus norvegicus (Norway rat)
C:Date: 26-Apr-1989 #sequence_revision 26-Apr-1989 #text_change 16-Jul-1999
C:Accession: A45882; A31278
R:McKnight, A.J.; Mason, D.W.; Barclay, A.N.
Immunogenetics 30, 145-147, 1989
A:Title: Sequence of rat interleukin 2 and anomalous binding of a mouse interleukin 2 cDNA
A:Reference number: A45882; MUID:89339608; PMID:2788130
A:Accession: A45882
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-155 <MCK>
A:Cross-references: GB:M22899; NID:g204909; PIDN:AAA41427.1; PID:g204910
C:Superfamily: interleukin-2
C:Keywords: cytokine; glycoprotein; growth factor; immunoregulation; T-cell

Query Match
Best Local Similarity 63.4%; Score 97; DB 2; Length 155;
Matches 20; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 APTSSSTKKTQLEHLLKQLMILNGINN 31
DB 21 APTSSPAKETQLEHLLKQLMILNGIDN 51

RESULT 5
S16241
interleukin-2 precursor - pig
N:Alternate names: IL-2; T-cell growth factor
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 16-Jul-1999
C:Accession: S16241; S15473
R:Goodall, J.C.; Emery, D.C.; Bailey, M.; English, L.S.; Hall, L.
Biochim. Biophys. Acta 1089, 257-258, 1991
A:Title: cDNA cloning of porcine interleukin 2 by polymerase chain reaction.
A:Reference number: S16241; MUID:91274360; PMID:2054386
A:Accession: S16241
A:Molecule type: mRNA
A:Residues: 1-154 <GOO>
A:Cross-references: EMBL:X56750; NID:g1991; PIDN:CAA40071.1; PID:g1992
R:Lefevre, F.
submitted to the EMBL Data Library, March 1991
A:Description: Molecular cloning of porcine interleukin 2 cDNA by the polymerase chain reaction
A:Reference number: S15473
A:Accession: S15473
A:Molecule type: mRNA
A:Residues: 1-154 <LEP>
A:Cross-references: EMBL:X58428; NID:g2068; PIDN:CAA41330.1; PID:g2069
C:Superfamily: interleukin-2
C:Keywords: cytokine; glycoprotein; growth factor; immunoregulation; T-cell
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-154/Product: interleukin-2 #status predicted <MAT>

Query Match
Best Local Similarity 62.7%; Score 96; DB 2; Length 154;
Matches 20; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 APTSSSTKKTQLEHLLKQLMILNGINN 31
DB 21 APTSSSTKKTQLEHLLKQLMILNGINN 51

RESULT 6
S33509
interleukin-2 - Mongolian jird
C:Species: Meriones unguiculatus (Mongolian jird)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Jul-1999
C:Accession: S33509
R:Mal, Z.; Klei, T.; Horohov, D.
submitted to the EMBL Data Library, October 1992
A:Description: Cross-species PCR cloning of Jird (Meriones unguiculatus) interleukin-2
A:Reference number: S33509
A:Accession: S33509
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-155 <MAT>
A:Cross-references: EMBL:X68779; NID:g577588; PIDN:CAA48679.1; PID:g311638
C:Superfamily: interleukin-2

Query Match
Best Local Similarity 62.1%; Score 95; DB 2; Length 155;
Matches 20; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

QY 1 APTSSSTKKTQLEHLLKQLMILNGINN 31
DB 21 APTSSPAKEAQYQLLELLDQLLRGINNY 51

RESULT 7
S31391
interleukin-2 precursor - horse
C:Species: Equus caballus (domestic horse)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
C:Accession: S31391
R:Tavernor, A.S.; Butcher, G.W.
submitted to the EMBL Data Library, November 1992
A:Description: cDNA cloning of equine interleukin-2 by polymerase chain reaction.
A:Reference number: S31391
A:Accession: S31391
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-149 <TAV>
A:Cross-references: EMBL:X69393; NID:g1076; PIDN:CAA49190.1; PID:g1077
C:Superfamily: interleukin-2

Query Match
Best Local Similarity 55.6%; Score 85; DB 2; Length 149;
Matches 16; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 1 APTSSSTKKTQLEHLLKQLMILNGINN 30
DB 21 APTSSSKRETQQLKQLMDLLEGVNN 50

RESULT 8
S38662
interleukin-2 - goat
C:Species: Capra aegagrus hircus (domestic goat)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Jul-1999
C:Accession: S38662
R:Rimstad, E.
submitted to the EMBL Data Library, November 1993
A:Description: The molecular cloning and expression of caprine interleukin 2.
A:Reference number: S38662
A:Accession: S38662
A>Status: preliminary

A:Molecule type: mRNA
A:Residues: 1-155 <RIM>
A:Cross-references: EMBL:X76063; NID:g416002; PIDN:CAA53664.1; PID:g416003
C:Superfamily: Interleukin-2

Query Match 47.1%; Score 72; DB 2; Length 155;
Best Local Similarity 50.0%; Pred. No. 0.0045;
Matches 15; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 1 APTSSSTKKTQLQLEHLLKLQMLINGINN 30
||||||| |::: ||| ||::: | |
Db 21 APTSSSTGNTMKVKSLLLDLQLLEKVK 50

RESULT 9

S11488
Interleukin-2 precursor - sheep
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999
C:Accession: S11488; S13102; S15517
R:Goodall, J.C.; Emery, D.C.; Perry, A.C.F.; English, L.S.; Hall, L.
Nucleic Acids Res. 18, 5883, 1990
A:Title: cDNA cloning of ovine interleukin 2 by PCR.
A:Reference number: S11488; MUID:91016933; PMID:2216781
A:Accession: S11488
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-155 <GOO>
A:Cross-references: EMBL:X53934; NID:g1281; PIDN:CAA37881.1; PID:g1282
R:Seow, H.F.; Rothel, J.S.; Raoford, A.J.; Wood, P.R.
Nucleic Acids Res. 18, 7175, 1990
A:Title: The molecular cloning of ovine interleukin 2 gene by the polymerase chain reaction.
A:Reference number: S13102; MUID:91088336; PMID:2263496
A:Accession: S13102
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-5, 'L', '7', '155 <SEO>
A:Cross-references: EMBL:X55641; NID:g1810; PIDN:CAA39165.1; PID:g1811
R:Bujdosó, R.; Williamson, M.L.; Sargan, D.R.; Hein, W.H.; McConnell, I.
submitted to the EMBL Data Library, April 1991
A:Reference number: S15517
A:Accession: S15517
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 21-153 <BUJ>
A:Cross-references: EMBL:X60148
C:Superfamily: Interleukin-2

Query Match 47.1%; Score 72; DB 2; Length 155;
Best Local Similarity 50.0%; Pred. No. 0.0045;
Matches 15; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 1 APTSSSTKKTQLQLEHLLKLQMLINGINN 30
||||||| |::: ||| ||::: | |
Db 21 APTSSSTGNTMKVKSLLLDLQLLEKVK 50

RESULT 10

I45913
Interleukin-2 precursor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 16-Jul-1999
C:Accession: I45913; S21470; S20761
R:Carretti, D.P.; McKereghan, K.; Larsen, A.; Cantrell, M.A.; Anderson, D.; Gillis, S.; Proc. Natl. Acad. Sci. U.S.A. 83, 3223-3227, 1986
A:Title: Cloning, sequence, and expression of bovine interleukin 2.
A:Reference number: I45913; MUID:86205869; PMID:3517854
A:Accession: I45913
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-155 <CER>
A:Cross-references: GB:W12791; NID:g163204; PIDN:AAA30586.1; PID:g163205
R:Anikeeva, N.N.; Vinogradova, T.V.; Votoshin, O.N.

submitted to the EMBL Data Library, December 1989
A:Reference number: S21470
A:Accession: S21470
A:Molecule type: DNA
A:Residues: 1-22 <AN2>
A:Cross-references: EMBL:X17201; NID:g452; PIDN:CAA35062.1; PID:g453
C:Genetics:
A:Gene: IL-2
C:Superfamily: Interleukin-2

C:Keywords: cytokine; glycoprotein; growth factor; immunoregulation; lymphokine; T-ce

Query Match 47.1%; Score 72; DB 2; Length 155;
Best Local Similarity 50.0%; Pred. No. 0.0045;
Matches 15; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 1 APTSSSTKKTQLQLEHLLKLQMLINGINN 30
||||||| |::: ||| ||::: | |
Db 21 APTSSSTGNTMKVKSLLLDLQLLEKVK 50

RESULT 11

S37289
Interleukin-2 precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
C:Accession: S37289; S27205; S36162; S24936
R:Todd, J.A.
submitted to the EMBL Data Library, April 1993
A:Reference number: S37289
A:Accession: S37289
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-169 <TOD>
A:Cross-references: EMBL:X73040
R:Matesanz, F.; Alcina, A.; Pellicer, A.
Biochim. Biophys. Acta 1132, 335-336, 1992
A:Title: A new cDNA sequence for the murine interleukin-2 gene.
A:Reference number: S27205; MUID:93041941; PMID:1420317
A:Accession: S27205
A:Molecule type: mRNA
A:Residues: 1-63 <MATE>
A:Cross-references: EMBL:X66058; NID:g52725; PIDN:CAA46854.1; PID:g52726
R:Ghosh, S.; Palmer, S.M.; Rodrigues, N.R.; Cordell, H.J.; Hearne, C.M.; Cornall, R.J.
Nature Genet. 4, 404-409, 1993
A:Title: Polygenic control of autoimmune diabetes in nonobese diabetic mice.
A:Reference number: S36162; MUID:94004970; PMID:8401590
A:Accession: S36162
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-50 <GHO>
A:Cross-references: EMBL:X73040
C:Superfamily: Interleukin-2
C:Keywords: cytokine; glycoprotein; growth factor; lymphokine; T-cell
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-63/Product: interleukin-2 #status predicted <NAT>

Query Match 45.1%; Score 69; DB 2; Length 169;
Best Local Similarity 45.9%; Pred. No. 0.014;
Matches 17; Conservative 6; Mismatches 8; Indels 6; Gaps 1;

QY 1 APTSSSTKKTQLQ-----LEHLLKLQMLINGINN 31
:|||||: |::: ||| ||::: | |
Db 29 SPTSSSTAQAQQQQQQQHQHLEQLLMDQLLELRMEY 65

RESULT 12

ICMS2
Interleukin-2 precursor - mouse
N:Alternate names: IL-2; T-cell growth factor (TCGF)
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 21-Jul-2000
C:Accession: A93550; A54490; A94084; I48597; A01850; I84713
R:Fuse, A.; Fujita, T.; Yasumitsu, H.; Kashima, N.; Hasegawa, K.; Taniguchi, T.

Nucleic Acids Res. 12, 9323-9331, 1984
A:Title: Organization and structure of the mouse interleukin-2 gene.
A:Reference number: A93550; MUID:85087940; PMID:6240025
A:Accession: A93550
A:Molecule type: DNA
A:Residues: 1-169 <FUS>
R:Degraive, W.; Simons, G.; Devos, R.; Plaetinck, G.; Remaut, E.; Tavernier, J.; Fiers, W.
Mol. Biol. Rep. 11, 57-61, 1986
A:Title: Cloning and structure of a mouse interleukin-2 chromosomal gene.
A:Reference number: A54490; MUID:86118396; PMID:3003564
A:Accession: A54490
A:Molecule type: DNA
A:Residues: 1-169 <DEG>
A:Cross-references: GB:M16760
R:Yokota, T.; Arai, N.; Lee, F.; Rennick, D.; Mosmann, T.; Arai, K.
Proc. Natl. Acad. Sci. U.S.A. 82, 68-72, 1985
A:Title: Use of a cDNA expression vector for isolation of mouse interleukin 2 cDNA clone
A:Reference number: A94064; MUID:85113172; PMID:3918306
A:Accession: A94064
A:Molecule type: mRNA
A:Residues: 1-169 <YOK>
A:Cross-references: GB:K02292; NID:g198330; PIDN:AAA39289.1; PID:g309404
R:Kashima, N.; Nishi-Takaoka, C.; Fujita, T.; Taki, S.; Yamada, G.; Hamuro, J.; Taniguchi
Nature 313, 402-404, 1985
A:Title: Unique structure of murine interleukin-2 as deduced from cloned cDNAs.
A:Reference number: I48597; MUID:85111148; PMID:2578624
A:Accession: I48597
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-169 <RES>
A:Cross-references: EMBL:X01772; GB:K02797; NID:g52663; PIDN:CAA25909.1; PID:g758159
C:Comment: Produced by T-cells in response to antigenic or mitogenic stimulation, this p
C:Genetics:
A:Introns: 63/3; 83/3; 132/3
C:Superfamily: interleukin-2
C:Keywords: cytokine; glycoprotein; growth factor; immunoregulation; lymphokine; T-cell
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-169/Product: interleukin-2 #status predicted <NAT>
F:23/Binding site: carbohydrate (Thr) (covalent) #status predicted
F:92-140/Disulfide bonds: #status predicted

Query Match 41.8%; Score 64; DB 1; Length 169;
Best Local Similarity 37.8%; Pred. No. 0.072; Indels 14; Gaps 1;
Matches 17; Conservative 6; Mismatches 8; Indels 14; Gaps 1;
QY 1 APTSSST-----KKTLQLEHLLKLQMLGINNY 31
DB 21 APTSSSTSTAEAAQQQQQQQQHLEQLLMDLQELLRMENY 65
|||||||
::: |||||::: ||
DB 21 APTSSSTSTAEAAQQQQQQQQHLEQLLMDLQELLRMENY 65

RESULT 13
H64307
hypothetical protein MJ0064 - Methanococcus jannaschii
C:Species: Methanococcus jannaschii
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C:Accession: H64307
R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
; Reich, C.L.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;
rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A:Authors: Kalne, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.
A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii.
A:Reference number: A64300; MUID:96337999; PMID:8688087
A:Accession: H64307
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-189 <BUL>
A:Cross-references: GB:U67464; GB:I77117; NID:g1590852; PIDN:AAB98051.1; PID:g1590855; I
C:Genetics:
A:Map position: FOR61888-62457
A:Start codon: GTG

Query Match 39.9%; Score 61; DB 2; Length 189;

Best Local Similarity 37.9%; Pred. No. 0.22;
Matches 11; Conservative 10; Mismatches 8; Indels 0; Gaps 0;
QY 3 TSSSTKTLQLEHLLKLQMLGINNY 31
DB 22 SSSSVLEIVLEIITKLNLISEINNY 50
|||||::: ||::: ||||
::: ||::: ||::: ||||

RESULT 14
GNLJG4
HIV-1 retropepsin (EC 3.4.23.16) - simian immunodeficiency virus (African green monkey
N:Contains: endonuclease (EC 3.1.-.-); retropepsin (EC 3.4.23.16); RNA-directed DNA p
C:Species: simian immunodeficiency virus, SIV
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 03-Jun-2002
C:Accession: B30045
R:Fukasawa, M.; Miura, T.; Hasegawa, A.; Morikawa, S.; Tsujimoto, H.; Miki, K.; Kitam
Nature 333, 457-461, 1988
A:Title: Sequence of simian immunodeficiency virus from African green monkey, a new m
A:Reference number: A30045; MUID:88232906; PMID:3374586
A:Accession: B30045
A:Molecule type: DNA
A:Residues: 1-1061 <FUK>
A:Cross-references: EMBL:X07805; NID:g61748; PID:g1335593
C:Comment: Specific enzymatic cleavages may yield mature proteins including protease,
C:Genetics:
A:Gene: pol
C:Superfamily: pol polyprotein
C:Keywords: aspartic proteinase; hydrolase; nucleotidyltransferase; polypeptide; reve
F:111-210/Product: retropepsin #status predicted <RPP>
F:134/Active site: Asp (shared with dimeric partner) #status predicted

Query Match 35.3%; Score 54; DB 1; Length 1061;
Best Local Similarity 58.8%; Pred. No. 15;
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 10 TQLQLEHLLKLQMLIN 26
DB 976 TLEIQLQTKIQLIN 992
|||||::: ||::: ||||
::: |||||::: |||||

RESULT 15
SI2169
isopenicillin N acyltransferase (EC 2.3.1.-) - Emericella nidulans
N:Alternate names: acyl coenzyme A-6-aminopenicillanic acid acyltransferase; acyltran
C:Species: Emericella nidulans, Aspergillus nidulans
C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000
C:Accession: SI2169; A36142; S09090
R:Montenegro, E.; Barredo, J.L.; Gutierrez, S.; Diez, B.; Alvarez, E.; Martin, J.F.
Mol. Gen. Genet. 221, 322-330, 1990
A:Title: Cloning, characterization of the acyl-CoA:6-amino penicillanic acid acyltran
A:Reference number: SI2169; MUID:90340281; PMID:2166227
A:Accession: SI2169
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-357 <MON>
A:Cross-references: EMBL:X53310; NID:g23378; PIDN:CAA37394.1; PID:g23379
R:Tobin, M.B.; Fleming, M.D.; Skatrud, P.L.; Miller, J.R.
J. Bacteriol. 172, 5908-5914, 1990
A:Title: Molecular characterization of the acyl-coenzyme A:isopenicillin N acyltransf
herichia coli.
A:Reference number: A36142; MUID:91008967; PMID:2120195
A:Accession: A36142
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-357 <TOB>
A:Cross-references: GB:M58293; NID:g167999; PIDN:AAA33287.1; PID:g168000
R:Whiteman, P.A.; Abraham, E.P.; Baldwin, J.E.; Fleming, M.D.; Schofield, C.J.; Suthe
FEBS Lett. 262, 342-344, 1990
A:Title: Acyl coenzyme A: 6-aminopenicillanic acid acyltransferase from Penicillium c
A:Reference number: S09089; MUID:90242961; PMID:2110531
A:Accession: S09090
A:Molecule type: protein
A:Residues: 103-122 <WHI>

C;Genetics:
A;Introns: 12/3; 71/1; 121/3
C;Keywords: acyltransferase
Query Match 34.6%; Score 53; DB 2; Length 357;
Best Local Similarity 52.6%; Pred. No. 6.5;
Matches 10; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
Qy 7 TTKTQLQLEHLLKIQMIL 25
 |||||:| | | :| : :
Db 40 TTKTQAELEQLLEQVM 58

Search completed: February 20, 2003, 10:07:25
Job time : 29.0476 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 20, 2003, 10:01:02 ; Search time 6.88889 Seconds
(without alignments)
186.643 Million cell updates/sec

Title: US-09-776-781-8
Perfect score: 153
Sequence: 1 APTSSSTKTKTQLQLHLLKQLMLNINNY 31

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	147	96.1	153	1 IL2_HUMAN	P01585 homo sapien
2	147	96.1	154	1 IL2_MACFA	Q29615 macaca fasc
3	147	96.1	154	1 IL2_MACMU	P31498 macaca mula
4	142	92.8	154	1 IL2_CERTO	P46649 cercopithec
5	116	75.8	154	1 IL2_MIRAN	O62641 mirounga an
6	107.5	70.3	155	1 IL2_CANFA	Q29416 canis famil
7	107	69.9	153	1 IL2_RABIT	O77620 oryctolagus
8	107	69.9	154	1 IL2_FELCA	Q07885 felis silve
9	97	63.4	155	1 IL2_RAT	P17108 rattus norv
10	96	62.7	154	1 IL2_PIG	P26891 sus scrofa
11	95	62.1	155	1 IL2_MERUN	Q08081 meriones un
12	88	57.5	152	1 IL2_ORCOR	O97513 orcinus orc
13	85	55.6	149	1 IL2_HORSE	P37997 equus cabal
14	72	47.1	155	1 IL2_BOVIN	P05016 bos taurus
15	72	47.1	155	1 IL2_CAPHI	P36835 capra hircu
16	72	47.1	155	1 IL2_SHEEP	P19114 ovis aries
17	72	47.1	162	1 IL2_CEREL	P51747 cervus elap
18	64.5	42.2	166	1 IL2_MUSSP	Q08867 mus spretus
19	64	41.8	169	1 IL2_MOUSE	P04351 mus musculu
20	61	39.9	189	1 Y064_METJA	Q60376 methanococc
21	56	36.6	1046	1 POL_SIVAG	P27980 simian immu
22	54	35.3	1061	1 POL_SIVAT	P05895 simian immu
23	53	34.6	357	1 AAAA_EMENI	P21133 emericecella
24	51.5	33.7	415	1 CGA2_XENLA	P47827 xenopus lae
25	50.5	33.0	741	1 RN5A_HUMAN	Q05823 homo sapien
26	48.5	31.7	452	1 TRPC_HELPY	Q25867 helicobacte
27	47.5	31.0	150	1 RNK6_SALSC	O46529 salmiri sci
28	47.5	31.0	150	1 RNK6_BOVIN	P08904 bos taurus
29	47	30.7	257	1 ABCX_GALSU	P35020 galdieria s
30	47	30.7	406	1 CGA2_BOVIN	P30274 bos taurus
31	47	30.7	421	1 CGA1_MOUSE	Q61456 mus musculu
32	47	30.7	432	1 CGA2_HUMAN	P20248 homo sapien
33	47	30.7	465	1 CGA1_HUMAN	P78396 homo sapien

ALIGNMENTS					RESULTS				
ID	IL2_HUMAN	STANDARD;	PRT;	153 AA.	ID	IL2_HUMAN	STANDARD;	PRT;	153 AA.
AC	P01585;				34	47	30.7	943	1 YLM5_CABEL
DT	21-JUL-1986 (Rel. 01, Created)				35	47	30.7	1492	1 CFTR_SQUAC
DT	21-JUL-1986 (Rel. 01, Last sequence update)				36	46.5	30.4	989	1 T100_HUMAN
DT	15-JUN-2002 (Rel. 41, Last annotation update)				37	46	30.1	532	1 G6PI_BORBU
DE	Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF)				38	46	30.1	746	1 PCAP_HUMAN
DE	(Aldelesleukin).				39	46	30.1	792	1 PCAP_MOUSE
GN	IL2.				40	45	29.4	81	1 EX7S_PASMU
OS	Homo sapiens (Human), and				41	45	29.4	368	1 LEU3_NEUCR
OS	Hylobates lar (Common gibbon).				42	45	29.4	479	1 ZW10_DROPS
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				43	45	29.4	903	1 MSPI_SCHPO
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				44	45	29.4	1019	1 POLSIVSA
OX	NCBI_TaxID=9606, 9580;				45	45	29.4	1158	1 ALAL_ARATH
RN	[1]								
RP	SEQUENCE FROM N.A.								
RC	SPECIES=Human;								
RC	MEDLINE=84247353; PubMed=6330695;								
RA	Holbrook N.J., Lieber M., Crabtree G.R.;								
RT	"DNA sequence of the 5' flanking region of the human interleukin 2 gene: homologues with adult T-cell leukemia virus.";								
RL	Nucleic Acids Res. 12:5005-5013(1984).								
RN	[2]								
RP	SEQUENCE FROM N.A.								
RC	SPECIES=Human;								
RC	MEDLINE=83167472; PubMed=6403867;								
RA	Taniguchi T., Matsui H., Fujita T., Takaoka C., Kashima N.,								
RA	Yoshimoto R., Hamuro J.;								
RT	"Structure and expression of a cloned cDNA for human interleukin-2.";								
RL	Nature 302:305-310(1983).								
RN	[3]								
RP	SEQUENCE FROM N.A.								
RC	SPECIES=Human;								
RC	MEDLINE=84023840; PubMed=6312994;								
RA	Maeda S., Nishino N., Obaru K., Mita S., Nomiya H., Shimada K.,								
RA	Fujimoto K., Teranishi T., Hirano T., Onoue K.;								
RT	"Cloning of interleukin 2 mRNAs from human tonsils.";								
RL	Biochem. Biophys. Res. Commun. 115:1040-1047(1983).								
RN	[4]								
RP	SEQUENCE FROM N.A.								
RC	SPECIES=Human;								
RC	MEDLINE=83246551; PubMed=6306584;								
RA	Devos R., Plaetinck G., Cheroutre H., Simons G., Degraeve W.,								
RA	Tavernier J., Remaut E., Fiers W.;								
RT	"Molecular cloning of human interleukin 2 cDNA and its expression in E. coli.";								
RL	Nucleic Acids Res. 11:4307-4323(1983).								
RN	[5]								
RP	SEQUENCE FROM N.A.								
RC	SPECIES=Human;								
RC	MEDLINE=84170356; PubMed=6608729;								
RA	Holbrook N.J., Smith K.A., Fornace A.J. Jr., Comeau C.M.,								
RA	Wiskocil R.L., Crabtree G.R.;								
RT	"T-cell growth factor: complete nucleotide sequence and organization of the gene in normal and malignant cells.";								

P34408 caenorhabdi
P26362 squalus aca
O75448 homo sapien
O51672 borrelia bu
O96rn5 homo sapien
Q224h2 mus musculu
Q9cna0 pasteurella
P34738 neurospora
O44218 drosophila
P87320 schizosacch
P12502 simian immu
P98204 arabidopsis

RL Proc. Natl. Acad. Sci. U.S.A. 81:1634-1638(1984).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Human;
 RX MEDLINE=84170243; PubMed=6324170;
 RA Fujita T., Takosaka C., Matsui H., Taniguchi T.;
 RT "Structure of the human interleukin 2 gene.";
 RL Proc. Natl. Acad. Sci. U.S.A. 80:7437-7441(1983).
 RN [7]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Human;
 RX MEDLINE=95239150; PubMed=7722480;
 RA Eisenberg O., Faber-Elman A., Lotan M., Schwartz M.;
 RT "Interleukin-2 transcripts in human and rodent brains: possible
 expression by astrocytes.";
 RL J. Neurochem. 64:1928-1936(1995).
 RN [8]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Human; TISSUE=Placenta;
 RX MEDLINE=96422299; PubMed=8824916;
 RA Chernicky C.L., Tan H., Burfeind P., Ilan J., Ilan J.;
 RT "Sequence of interleukin-2 isolated from human placental poly A+ RNA:
 possible role in maintenance of fetal allograft.";
 RL Mol. Reprod. Dev. 43:180-186(1996).
 RN [9]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Human;
 RX MEDLINE=92335891; PubMed=1631562;
 RA Nickerson D.A.; Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 RN [10]
 RP SEQUENCE OF 21-153 FROM N.A.
 RC SPECIES=Human;
 RX MEDLINE=89062420; PubMed=3264184;
 RA Weir M.P., Chaplin M.A., Wallace D.M., Dykes C.W., Hobden A.N.;
 RT "Structure-activity relationships of recombinant human interleukin
 2.";
 RL Biochemistry 27:6883-6892(1988).
 RN [11]
 RP SEQUENCE OF 1-69 FROM N.A.
 RC SPECIES=Human;
 RX MEDLINE=87064618; PubMed=3491296;
 RA Stebenliet U., Durand D.B., Bressler P., Holbrook N.J., Norris C.A.,
 RA Kamoun M., Kant J.A., Crabtree G.R.;
 RT "Promoter region of interleukin-2 gene undergoes chromatin structure
 changes and confers inducibility on chloramphenicol acetyltransferase
 gene during activation of T cells.";
 RL Mol. Cell. Biol. 6:3042-3049(1986).
 RN [12]
 RP SEQUENCE OF 1-68 FROM N.A.
 RC SPECIES=Human;
 RX MEDLINE=85038540; PubMed=6333684;
 RA Nishino N., Obaru K., Maeda S., Shimada K., Onoue K.;
 RA "Organization of the DNA regions flanking the human interleukin 2
 gene.";
 RL Biomed. Res. 6:197-205(1985).
 RN [13]
 RP SEQUENCE OF 21-153, DISULFIDE BOND, AND CARBOHYDRATE-LINKAGE SITE.
 RC SPECIES=Human;
 RX MEDLINE=85038540; PubMed=6333684;
 RA Robb R.J., Kutny R.M., Panico M., Morris H.R., Chowdhry V.;
 RA "Amino acid sequence and post-translational modification of human
 interleukin 2.";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:6486-6490(1984).
 RN [14]
 RP CARBOHYDRATE-LINKAGE SITE.
 RC SPECIES=Human;
 RX MEDLINE=9008901; PubMed=2793860;
 RA Conradt H.S., Nimtz M., Dittmar K.E.J., Lindenmaier W., Hoppe J.,
 RA Hauser H.;
 RT "Expression of human interleukin-2 in recombinant baby hamster
 kidney, Ltk+, and Chinese hamster ovary cells. Structure of O-linked
 carbohydrate chains and their location within the polypeptide.";
 RL J. Biol. Chem. 264:17368-17373(1989).

RN [15]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Human;
 RX MEDLINE=86042650; PubMed=3877307;
 RA Chen S.J., Holbrook N.J., Mitchell K.F., Vallone C.A.,
 RA Greengard J.S., Crabtree G.R., Lin Y.;
 RT "A viral long terminal repeat in the interleukin 2 gene of a cell
 line that constitutively produces interleukin 2.";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:7284-7288(1985).
 RN [16]
 RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
 RC SPECIES=Human;
 RX MEDLINE=88070646; PubMed=3500515;
 RA Brandhuber B.J., Boone T., Kenney W.C., McKay D.B.;
 RT "Three-dimensional structure of interleukin-2.";
 RL Science 238:1707-1709(1987).
 RN [17]
 RP X-RAY CRYSTALLOGRAPHY.
 RX MEDLINE=92335891; PubMed=1631562;
 RA Bazan J.F.;
 RT "Unraveling the structure of IL-2.";
 RL Science 257:410-412(1992).
 RN [18]
 RP RESPONSE TO ABOVE LETTER.
 RA McKay D.B.;
 RL Science 257:412-413(1992).
 RN [19]
 RP STRUCTURE BY NMR.
 RX MEDLINE=92379010; PubMed=1510960;
 RA Mott H.R., Driscoll P.C., Boyd J., Cooke R.M., Weir M.P.,
 RA Campbell I.D.;
 RT "Secondary structure of human interleukin 2 from 3D heteronuclear NMR
 experiments.";
 RL Biochemistry 31:7741-7744(1992).
 RN [20]
 RP 3D-STRUCTURE MODELING.
 RX MEDLINE=95111955; PubMed=7529123;
 RA Bamorough P., Hedgecock C.J., Richards W.G.;
 RT "The interleukin-2 and interleukin-4 receptors studied by molecular
 modelling.";
 RL Structure 2:839-851(1994).
 CC -|- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR
 MITOGENIC STIMULATION, THIS PROTEIN IS REQUIRED FOR T-CELL
 PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE
 IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-
 ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS.
 CC -|- SUBCELLULAR LOCATION: Secreted.
 CC -|- DISEASE: A FORM OF T-CELL ACUTE LYMPHOBLASTIC LEUKEMIA (T-ALL) IS
 CHARACTERIZED BY A CHROMOSOMAL TRANSLOCATION T(4;16)(Q26;P13)
 WHICH INVOLVES IL2 AND BCMA.
 CC -|- PHARMACEUTICAL: Available under the name Proleukin (Chiron). Used
 in patients with renal cell carcinoma or metastatic melanoma.
 CC -|- SIMILARITY: BELONGS TO THE IL-2 FAMILY.
 CC -|- DATABASE: NAME-R&D Systems' cytokine source book: IL2;
 WWW="http://www.rndsystems.com/asp/g_sitebuilder.asp?bodyid=206".

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 or send an email to license@isb-sib.ch).

CC EMBL; J00264; A048509.1;
 CC EMBL; X01586; CAA25742.1;
 CC EMBL; V00564; CAA23827.1;
 CC EMBL; X00695; CAA25292.1;
 CC EMBL; K02056; AAA98792.1;
 CC EMBL; M13879; AAA59141.1;
 CC EMBL; K03174; AAA35453.1;
 CC EMBL; S77834; AAD14283.2;
 CC EMBL; S82692; AAB46883.1;

Query Match 96.1%; Score 147; DB 1; Length 153;
 Best Local Similarity 96.8%; Pred. No. 4.3e-15;
 Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 APTSSSTKTKTQLEHLLKLQMLINGINNY 31
 |||||||
 DB 21 APTSSSTKTKTQLEHLLKLQMLINGINNY 51

RESULT 2

IL2_MACFA STANDARD; PRT; 154 AA.

AC Q29615;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
 GN IL2.
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
 OC Cercopitheidae; Macaca.
 OX NCBI_TaxID=9541;
 RN [1]
 RP SEQUENCE FROM N.A.

RC TISSUE-Peripheral blood;

RA Yabe M., Matsura Y., Tatsumi M.;

RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR

CC MITOGENIC STIMULATION, THIS PROTEIN IS REQUIRED FOR T-CELL

CC PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE

CC IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-

CC ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS (BY

CC SIMILARITY).

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- SIMILARITY: BELONGS TO THE IL-2 FAMILY.

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CC -----

DR EMBL; D63352; BAA09676.1; -.

DR HSSP; P01585; 3INK.

DR InterPro: IPR000779; Interleukin-2.

DR Pfam: PF00715; IL2; 1.

DR PRINTS; PR00265; INTERLEUKIN2.

DR ProDom; PD003649; Interleukin-2; 1.

DR SMART; SM00189; IL2; 1.

DR PROSITE; PS00424; INTERLEUKIN2; 1.

KW Cytokine; Glycoprotein; Immune response; Signal; Growth factor;

KW T-cell.

FT SIGNAL 1 20 BY SIMILARITY.

FT CHAIN 21 154 INTERLEUKIN-2.

FT CARBOHYD 23 23 O-LINKED (GALNAC. . .) (BY SIMILARITY).

FT DISULFID 78 126 BY SIMILARITY.

FT SEQUENCE 154 AA; 17686 MW; 7853FE62A5E4A49 CRC64;

Query Match 96.1%; Score 147; DB 1; Length 154;

Best Local Similarity 96.8%; Pred. No. 4.3e-15;

Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 APTSSSTKTKTQLEHLLKLQMLINGINNY 31

|||||

DB 21 APTSSSTKTKTQLEHLLKLQMLINGINNY 51

RESULT 3

IL2_MACMU

IL2_MACMU STANDARD; PRT; 154 AA.

P51498;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).

GN IL2.

OS Macaca mulatta (Rhesus macaque), and

OS Macaca nemestrina (Pig-tailed macaque).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;

OC Cercopitheidae; Macaca.

OX NCBI_TaxID=9544, 9545;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE-Blood;

RX MEDLINE=96003435; PubMed=7561102;

RA Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;

RT "Comparative sequence analysis of cytokine genes from human and

RT nonhuman primates.;"

RL J. Immunol. 155:3946-3954(1995).

CC -!- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR

CC MITOGENIC STIMULATION, THIS PROTEIN IS REQUIRED FOR T-CELL

CC PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE

CC IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-

CC ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS (BY

CC SIMILARITY).

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- SIMILARITY: BELONGS TO THE IL-2 FAMILY.

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CC -----

DR EMBL; U19847; AAB60400.1; -.

DR EMBL; U19852; AAB6714.1; -.

DR HSSP; P01585; 3INK.

DR InterPro: IPR000779; Interleukin-2.

DR Pfam: PF00715; IL2; 1.

DR PRINTS; PR00265; INTERLEUKIN2.

DR ProDom; PD003649; Interleukin-2; 1.

DR SMART; SM00189; IL2; 1.

DR PROSITE; PS00424; INTERLEUKIN2; 1.

KW Cytokine; Glycoprotein; Immune response; Signal; Growth factor;

KW T-cell.

FT SIGNAL 1 20 BY SIMILARITY.

FT CHAIN 21 154 INTERLEUKIN-2.

FT CARBOHYD 23 23 O-LINKED (GALNAC. . .) (BY SIMILARITY).

FT DISULFID 78 126 BY SIMILARITY.

FT SEQUENCE 154 AA; 17685 MW; 6AEB480F204BA49 CRC64;

Query Match 96.1%; Score 147; DB 1; Length 154;

Best Local Similarity 96.8%; Pred. No. 4.3e-15;

Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 APTSSSTKTKTQLEHLLKLQMLINGINNY 31

|||||

DB 21 APTSSSTKTKTQLEHLLKLQMLINGINNY 51

RESULT 4

IL2_CERTO

ID IL2_CERTO STANDARD; PRT; 154 AA.

AC P46649;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).

GN IL2.


```
CC ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE IL-2 FAMILY.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; L19402; AAA02865.1; -.
CC EMBL; L25408; AAA51431.1; -.
CC PIR; JN0598; JN0698.
CC HSSP; P01585; 3INK.
CC InterPro: IPR000779; Interleukin-2.
CC Pfam; PF00715; IL2; 1.
CC PRINTS; PR00265; INTERLEUKIN2.
CC PRODOM; PD003649; Interleukin-2; 1.
CC SMART; SM00189; IL2; 1.
CC PROSITE; PS00424; INTERLEUKIN_2; 1.
CC Cytokine; Glycoprotein; Immune response; Signal; Growth factor;
CC T-cell.
CC SIGNAL 1 20 BY SIMILARITY.
CC CHAIN 21 154 INTERLEUKIN-2.
CC DISULFID 78 126 BY SIMILARITY.
CC CARBOHYD 111 111 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CONFLICT 3 4 KI -> RM (IN REF. 2).
CC CONFLICT 150 150 F -> I (IN REF. 2).
CC SEQUENCE 154 AA; 17653 MW; 2E71E3BD89B965EF CRC64;

Query Match 69.9%; Score 107; DB 1; Length 154;
Best Local Similarity 70.0%; Pred. No. 4.7e-09;
Matches 21; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 APTSSSTKTKTQLEHLLKLMILNGINN 30
   |||||:||||| ||| ||| :|||:|||||
Db 21 APASSSTKTKTQLEHLLKLMILNGINN 50

RESULT 9
IL2_RAT
ID IL2_RAT STANDARD; PRT; 155 AA.
AC P17108;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
GN IL2 OR IL-2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89339608; PubMed=2788130;
RA McKnight A.J., Mason D.W., Barclay A.N.;
RT "Sequence of rat interleukin 2 and anomalous binding of a mouse
RT chain mRNA.";
RL Immunogenetics 30:145-147(1989).
CC -1- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR
CC MITOGENIC STIMULATION, THIS PROTEIN IS REQUIRED FOR T-CELL
CC PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE
CC IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-
CC ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE IL-2 FAMILY.
CC -----
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CC -----
CC EMBL; M22899; AAA41427.1; -.
CC PIR; A31278; A31278.
CC PIR; A45882; A45882.
CC HSSP; P01585; 3INK.
CC InterPro: IPR000779; Interleukin-2.
CC Pfam; PF00715; IL2; 1.
CC PRINTS; PR00265; INTERLEUKIN2.
CC PRODOM; PD003649; Interleukin-2; 1.
CC SMART; SM00189; IL2; 1.
CC PROSITE; PS00424; INTERLEUKIN_2; 1.
CC Cytokine; Glycoprotein; Immune response; Signal; Growth factor;
CC T-cell.
CC SIGNAL 1 20 BY SIMILARITY.
CC CHAIN 21 155 INTERLEUKIN-2.
CC CARBOHYD 23 23 O-LINKED (GALNAC. .) (BY SIMILARITY).
CC DISULFID 78 126 BY SIMILARITY.
CC SEQUENCE 155 AA; 17632 MW; 67A8554A73BF30A0 CRC64;

Query Match 63.4%; Score 97; DB 1; Length 155;
Best Local Similarity 64.5%; Pred. No. 1.5e-07;
Matches 20; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 APTSSSTKTKTQLEHLLKLMILNGINN 31
   |||||:||||| ||| ||| |||:|||||
Db 21 APTSSPAKETQQLLEQLLDLQVLLRGIDNY 51

RESULT 10
IL2_PIG
ID IL2_PIG STANDARD; PRT; 154 AA.
AC P26891;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
GN IL2.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=T-cell;
RX MEDLINE=91274360; PubMed=2054386;
RA Goodall J.C., Emery D.C., Bailey M., English L.S., Hall L.;
RT "cDNA cloning of porcine interleukin 2 by polymerase chain reaction.";
RL Biochim. Biophys. Acta 1089:257-258(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=T-cell;
RA Lefevre F.;
RL Submitted (MAY-1991) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Iwata H., Hasegawa A., Yamamoto M., Oida T., Endo Y., Inoue T.;
RT "Structure of the porcine chromosomal interleukin-2 gene.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR
CC MITOGENIC STIMULATION, THIS PROTEIN IS REQUIRED FOR T-CELL
CC PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE
CC IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-
CC ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE IL-2 FAMILY.
CC -----
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FT SIGNAL 1 20 BY SIMILARITY.
FT CHAIN 21 >152 INTERLEUKIN-2.
FT CARBOHYD 23 23 O-LINKED (GALNAC. . .) (BY SIMILARITY).
FT DISULFID 78 126 BY SIMILARITY.
FT NON_TER 152 152
SQ SEQUENCE 152 AA; 17424 MW; 308F91821ECCB764 CRC64;

Query Match 57.5%; Score 88; DB 1; Length 152;
Best Local Similarity 59.1%; Pred. No. 3.4e-06;
Matches 18; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 1 APTSSSTKKTQLQLEHLLKQLQMLINGINN 31
| | | | | : : : : | : : : | | | |
Db 21 APTSSSTNTKKQVSLQQLQLLLKEINNY 51

RESULT 13
IL2_HORSE
ID IL2_HORSE STANDARD; PRT; 149 AA.
AC P37997;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
GN IL2.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OC NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94160538; PubMed=8116217;
RA Vandergriff E.V., Horohov D.W.;
RT "Molecular cloning and expression of equine interleukin 2.";
RL Vet. Immunol. Immunopathol. 39:395-406(1993).
RN [2]
RP SEQUENCE FROM N.A.
RA Tavernor A.S., Allen W.R., Butcher G.W.;
RL Submitted (NOV-1992) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR
CC MITOGENIC STIMULATION. THIS PROTEIN IS REQUIRED FOR T-CELL
CC PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE
CC IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-
CC ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE IL-2 FAMILY.
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CC or send an email to licensee@isb-sib.ch).
CC -----
CC EMBL; L06009; AAA20134.1; -
CC EMBL; X69393; CAA49190.1; -
CC PIR; S31391; S31391.
CC HSP; P01585; 31NK.
DR InterPro: IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00265; INTERLEUKIN2.
DR PRODOM; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN2; 1.
KW Cytokine; Glycoprotein; Immune response; Signal; Growth factor;
KW T-cell.
FT SIGNAL 1 20 BY SIMILARITY.
FT CHAIN 21 149 INTERLEUKIN-2.
FT CARBOHYD 78 121 BY SIMILARITY.
FT DISULFID 23 23 O-LINKED (GALNAC. . .) (BY SIMILARITY).
FT CARBOHYD 106 106 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 3 3 R -> K (IN REF. 2).

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FT CONFLICT 8 8 S -> A (IN REF. 2).
FT CONFLICT 59 59 I -> M (IN REF. 2).
FT CONFLICT 125 125 N -> D (IN REF. 2).
FT CONFLICT 128 128 E -> G (IN REF. 2).
FT CONFLICT 145 145 I -> F (IN REF. 2).
FT CONFLICT 148 148 L -> M (IN REF. 2).
SQ SEQUENCE 149 AA; 17086 MW; 051BB8C47A0114FC CRC64;

Query Match 55.6%; Score 85; DB 1; Length 149;
Best Local Similarity 53.3%; Pred. No. 9.4e-06;
Matches 16; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

Qy 1 APTSSSTKKTQLQLEHLLKQLQMLINGINN 30
| | | | | : : : : | : : : | | | |
Db 21 APTSSSKRETQQLKQLQMDLKLLEGVNN 50

RESULT 14
IL2_BOVIN
ID IL2_BOVIN STANDARD; PRT; 155 AA.
AC P05016;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
GN IL2 OR IL-2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae.
OC Bovidae; Bovinae; Bos.
OC NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86205869; PubMed=3517854;
RA Carretti D.P., McKereghan K., Larsen A., Cantrell M.A., Anderson D.,
RA Gillis S., Cosman D., Baker P.E.;
RT "Cloning, sequence, and expression of bovine interleukin 2.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:3223-3227(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=86205870; PubMed=3486415;
RA Reeves R., Spies A.G., Nissen M.S., Buck C.D., Weinberg A.D.,
RA Barr P.J., Magnuson N.S., Magnuson J.A.;
RT "Molecular cloning of a functional bovine interleukin 2 cDNA.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:3228-3232(1986).
RN [3]
RP SEQUENCE OF 1-22 FROM N.A.
RC TISSUE=Thymus;
RA Anikeeva N.N., Vinogradova T.V., Votoshin O.N.;
RL Submitted (DEC-1989) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR
CC MITOGENIC STIMULATION. THIS PROTEIN IS REQUIRED FOR T-CELL
CC PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE
CC IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-
CC ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE IL-2 FAMILY.
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CC -----
CC EMBL; M12791; AAA30586.1; -
CC EMBL; M13204; AAA21143.1; ALT_INIT.
CC EMBL; X17201; CAA35062.1; -
CC EMBL; X52687; CAA36912.1; -
CC HSP; P01585; 31NK.
DR InterPro: IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.

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DR PRINTS: PR00265; INTERLEUKIN2.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
KW Cytokine; Glycoprotein; Immune response; Signal; Growth factor;
KW T-cell.
FT SIGNAL 1 20 BY SIMILARITY.
FT CHAIN 21 155 INTERLEUKIN-2.
FT DISULFID 79 127 BY SIMILARITY.
FT CARBOHYD 23 23 O-LINKED (GALNAC. . .) (BY SIMILARITY).
FT CONFLICT 66 66 V -> A (IN REF. 2).
SQ SEQUENCE 155 AA; 17627 MW; 816667DFEA052EDF CRC64;

Query Match 47.1%; Score 72; DB 1; Length 155;
Best Local Similarity 50.0%; Pred. No. 0.0009;
Matches 15; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 1 APTSSSTKKTQLQLEHLLKQLMILNGINN 30
DB 21 APTSSSTGNTMKVKSLLDLQLLEKVN 50

RESULT 15
IL2_CAPHI STANDARD; PRT; 155 AA.
AC P36835; P79156;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
GN IL2.
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Capra.
OX NCBI_TaxID=9925;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Rimstad E.;
RL Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Beyer J.C.; Cheevers W.P.;
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
CC !- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR
CC MITOGENIC STIMULATION, THIS PROTEIN IS REQUIRED FOR T-CELL
CC PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE
CC IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-
CC ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS.
CC !- SUBCELLULAR LOCATION: Secreted.
CC !- SIMILARITY: BELONGS TO THE IL-2 FAMILY.
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CC -----
DR EMBL; X76063; CAA53664.1; -.
DR EMBL; U34274; AAB38527.1; -.
DR PIR; S38662; S38662.
DR HSP; P01585; 3INK.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00265; INTERLEUKIN2.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
KW Cytokine; Glycoprotein; Immune response; Signal; Growth factor;
KW T-cell.

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FT SIGNAL 1 20 BY SIMILARITY.
FT CHAIN 21 155 INTERLEUKIN-2.
FT CARBOHYD 23 23 O-LINKED (GALNAC. . .) (BY SIMILARITY).
FT DISULFID 79 127 BY SIMILARITY.
FT CONFLICT 3 5 RMQ -> QIP (IN REF. 2).
FT CONFLICT 22 22 P -> T (IN REF. 2).
FT CONFLICT 30 30 T -> P (IN REF. 2).
FT CONFLICT 51 51 L -> P (IN REF. 2).
FT CONFLICT 71 71 D -> A (IN REF. 2).
FT CONFLICT 89 89 D -> E (IN REF. 2).
FT CONFLICT 99 99 R -> L (IN REF. 2).
FT CONFLICT 107 113 YMASLKG -> SMDNIKR (IN REF. 2).
FT CONFLICT 140 140 Q -> L (IN REF. 2).
FT CONFLICT 144 144 T -> I (IN REF. 2).
FT CONFLICT 154 154 L -> M (IN REF. 2).
SQ SEQUENCE 155 AA; 17703 MW; 90022DFBB6AF78DE CRC64;

Query Match 47.1%; Score 72; DB 1; Length 155;
Best Local Similarity 50.0%; Pred. No. 0.0009;
Matches 15; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 1 APTSSSTKKTQLQLEHLLKQLMILNGINN 30
DB 21 APTSSSTGNTMKVKSLLDLQLLEKVN 50

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Search completed: February 20, 2003, 10:05:24
Job time : 6.88889 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 20, 2003, 10:03:07 ; Search time 24.1111 Seconds
(without alignments)
264.918 Million cell updates/sec

Title: US-09-776-781-8
Perfect score: 153
Sequence: 1 APTSSSTKTKTQLEHLLKQLMILNGINNY 31

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: SP_TREMBL_21.*
- 2: SP_Archaea.*
- 3: SP_Bacteria.*
- 4: SP_Fungi.*
- 5: SP_Human.*
- 6: SP_Invertebrate.*
- 7: SP_Mammal.*
- 8: SP_MHC.*
- 9: SP_Organelle.*
- 10: SP_Phage.*
- 11: SP_Plant.*
- 12: SP_Rodent.*
- 13: SP_Virus.*
- 14: SP_Unclassified.*
- 15: SP_Virus.*
- 16: SP_Bacteriap.*
- 17: SP_Archeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	147	96.1	150	4	Q9C001	Q9C001 homo sapien
2	145	94.8	154	6	Q9XS38	Q9XS38 papio hamad
3	135.5	88.6	156	4	Q13169	Q13169 homo sapien
4	134	87.6	139	4	Q16334	Q16334 homo sapien
5	108.5	70.9	155	6	Q9XT83	Q9XT83 halichoerus
6	107.5	70.3	66	6	Q9BG74	Q9BG74 canis famil
7	107	69.9	75	6	Q9TV12	Q9TV12 canis famil
8	106	69.3	155	11	Q923T2	Q923T2 sigmodon hi
9	103	67.3	138	11	Q70329	Q70329 mesocricetu
10	99	64.7	133	6	Q9MZ99	Q9MZ99 oryctolagus
11	84	54.9	23	4	Q9UCF5	Q9UCF5 homo sapien
12	78	51.0	154	6	Q9XT84	Q9XT84 delphinapte
13	75	49.0	152	11	Q88210	Q88210 cavia porce
14	72	47.1	69	6	Q9GJRA	Q9GJRA ovis aries
15	72	47.1	155	6	Q9GL83	Q9GL83 capra hircu
16	72	47.1	155	6	Q95KP3	Q95KP3 bubalus bub

17	69	45.1	39	6	Q9BG73	Q9BG73 canis famil
18	69	45.1	150	11	Q90291	Q90291 mus musculu
19	69	45.1	169	11	Q90US8	Q90US8 mus musculu
20	67	43.8	150	11	P70294	P70294 mus musculu
21	62.5	40.8	159	11	P70293	P70293 mus musculu
22	60.5	39.5	155	11	P70292	P70292 mus musculu
23	56	36.6	300	2	Q8VM37	Q8VM37 coxiellia bu
24	56	36.6	348	12	Q9DHS6	Q9DHS6 yaba-like d
25	53	34.6	452	10	Q9PYU2	Q9PYU2 xestia c-ni
26	53	34.6	452	10	Q9ZV75	Q9ZV75 arabidopsis
27	52	34.0	116	6	Q29138	Q29138 trichechus
28	52	34.0	478	17	Q8TLR6	Q8TLR6 methanosarc
29	51	33.3	517	16	Q8R688	Q8R688 thermoanar
30	51	33.3	737	16	Q9KTG5	Q9KTG5 vibrio chol
31	51	33.3	866	16	Q25517	Q25517 helicobacte
32	51	33.3	875	16	Q9ZKZ8	Q9ZKZ8 helicobacte
33	50	32.7	95	2	Q9F8U6	Q9F8U6 streptomyce
34	50	32.7	304	16	Q930K5	Q930K5 rhizobium m
35	50	32.7	543	16	Q9KSF8	Q9KSF8 vibrio chol
36	49.5	32.4	104	10	Q9FSQ4	Q9FSQ4 oryza sativ
37	49.5	32.4	367	10	Q9SIF5	Q9SIF5 arabidopsis
38	49.5	32.4	474	10	Q06376	Q06376 brassica na
39	49	32.0	145	16	Q9KAW0	Q9KAW0 bacillus ha
40	48.5	31.7	366	16	Q98G42	Q98G42 rhizobium l
41	48	31.4	311	16	Q9CLL6	Q9CLL6 pasteurella
42	48	31.4	398	16	Q50911	Q50911 borrelia bu
43	48	31.4	441	16	Q928V0	Q928V0 listeria in
44	48	31.4	441	16	Q69192	Q69192 listeria mo
45	48	31.4	765	16	P74599	P74599 synechocyst

ALIGNMENTS

RESULT 1

Q9C001 PRELIMINARY; PRT; 150 AA.
AC Q9C001; TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Interleukin-2 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Cranata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20545237; PubMed=11093171;
RA Matesanz F., Delgado C., Fresno M., Alcina A.;
RT "Allelic selection of human IL-2 gene."
RL Eur. J. Immunol. 30:3516-3521(2000).
DR EMBL; AF228636; AAG53575.1; -
DR HSSP; P01585; 3INK
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PD00265; INTERLEUKIN2.
DR PRODOM; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
FT NON_TER 150 150
SQ SEQUENCE 150 AA; 17312 MW; BF25860F8436ACE5 CRC64;

Query Match 96.1%; Score 147; DB 4; Length 150;

Best Local Similarity 96.8%; Pred. No. 4.3e-14;

Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 APTSSSTKTKTQLEHLLKQLMILNGINNY 31

Db 21 APTSSSTKTKTQLEHLLKQLMILNGINNY 51

RESULT 2

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Q9XS38
ID Q9XS38 PRELIMINARY; PRT; 154 AA.
AC Q9XS38;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
DE IL-2.
OS Papio hamadryas (Hamadryas baboon),
OS Aotus lemurinus (Northern gray-necked night monkey),
OS Aotus nancymae (Owl monkey),
OS Aotus nigriceps (black-headed night monkey), and
OS Aotus vociferans (noisy night monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Papio.
ON NCBI_TaxID=9557, 43147, 37293, 57175, 57176;
RN [1]
RP SEQUENCE FROM N.A.
RA Murillo L.A., Hernandez E., Echeverry S.J., Mendez J.A., Moreno A.,
RA Patarroyo M.E.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U88365; AAD41538.1; -
DR EMBL; U88364; AAD41534.1; -
DR EMBL; U88361; AAD41535.1; -
DR EMBL; U88363; AAD41536.1; -
DR EMBL; U88362; AAD41537.1; -
DR HSSP; P01585; 3INK.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00265; INTERLEUKIN2.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
SQ SEQUENCE 154 AA; 17675 MW; AB752ABBADA96469 CRC64;

Query Match 94.88; Score 145; DB 6; Length 154;
Best Local Similarity 93.58; Pred. No. 8.7e-14;
Matches 29; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 APTSSSTKKTQQLQLEHLLKLQMLINGINNY 31
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Db 21 APTSSSTKKTQQLQLEHLLKLQMLINGINNY 51

RESULT 3
Q13169 PRELIMINARY; PRT; 156 AA.
ID Q13169
AC Q13169;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Interleukin 2.
GN IL2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
ON NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Xu D., Wu Y., Chen J., Yu L., Zhong M., Hui Y., Qu H.;
RT "Expression of human IL-2 from gene transferred mouse melanoma cells
RT and its effect on the growth of mouse melanoma.";
RL Chung-Hua Min Kuo Wei Sheng Wu Chi Mien I Hsueh Tsa Chih
RL 13:78-82(1993).
RN [2]
RP SEQUENCE FROM N.A.
RA Xu L.;
RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U25676; AAA70092.1; -
DR HSSP; P01585; 3INK.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00265; INTERLEUKIN2.

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DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
SQ SEQUENCE 156 AA; 18002 MW; 8E0452D43B336389 CRC64;

Query Match 88.68; Score 135.5; DB 4; Length 156;
Best Local Similarity 88.28; Pred. No. 2.3e-12;
Matches 30; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

QY 1 APTSSS---TKKTLQLEHLLKLQMLINGINNY 31
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Db 21 APTSSSTKKTQQLQLEHLLKLQMLINGINNY 54

RESULT 4
Q16334 PRELIMINARY; PRT; 139 AA.
ID Q16334
AC Q16334;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
DE IL-2 protein (Fragment).
GN IL-2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
ON NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Eizenberg O., Faber-Elman A., Lotan M., Schwartz M.;
RT "Interleukin-2 transcripts in human and rodent brains: possible
RT expression by astrocytes.";
RL J. Neurochem. 64:1928-1936(1995).
DR EMBL; S77835; AAD14264.1; -
DR HSSP; P01585; 3INK.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00265; INTERLEUKIN2.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
FT NON_TER
SQ SEQUENCE 139 AA; 15986 MW; 731FBA406D0C63C5 CRC64;

Query Match 87.68; Score 134; DB 4; Length 139;
Best Local Similarity 90.38; Pred. No. 3.5e-12;
Matches 28; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 APTSSSTKKTQQLQLEHLLKLQMLINGINNY 31
|||||
Db 17 APTSSSTKKTQQLQLEHLLKLQMLINGINNY 47

RESULT 5
Q9XT83 PRELIMINARY; PRT; 155 AA.
ID Q9XT83
AC Q9XT83;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Interleukin 2.
OS Halichoerus grypus (Gray seal).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Pinnipedia; Phocidae; Halichoerus.
ON NCBI_TaxID=9711;
RN [1]
RP SEQUENCE FROM N.A.
RA St-Laurent G., Belliveau C., Archambault D.;
RT "Molecular cloning and phylogenetic analysis of beluga whale
RT (Delphinapterus leucas) and grey seal (Halichoerus grypus) interleukin
RT 2.";

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RC TISSUE=SPLEEN;
RX MEDLINE=98233044; PubMed=9573100;
RA Melby P.C., Tryon V.V., Chandrasekar B., Freeman G.L.;
RT "Cloning of Syrian hamster (Mesocricetus auratus) cytokine cDNAs and
RT analysis of cytokine mRNA expression in experimental visceral
RT leishmaniasis.";
RL Infect. Immun. 66:2135-2142(1998).
DR EMBL; AF046212; AAC40097.1; -.
DR HSSP; P01585; 3INK.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00265; INTERLEUKIN2.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
DR NON_TER 1
FT NON_TER 138
SQ SEQUENCE 138 AA; 15739 MW; 351032995B670779 CRC64;

Query Match 67.3%; Score 103; DB 11; Length 138;
Best Local Similarity 71.0%; Pred. No. 1.5e-07;
Matches 22; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy 1 APTSSSTKKTQLQLEHLLKLQMLNGINNY 31
Db 14 APTSSSKKETQQLRLQLDLQLQLKGINNY 44

RESULT 10
Q9WZR9 PRELIMINARY; PRT; 133 AA.
AC Q9WZR9;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Interleukin 2 variant IL2delta2.
GN IL-2.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SPLEEN, AND LYMPH NODE;
RX MEDLINE=20304414; PubMed=10843729;
RA Perkins H.D., van Leeuwen B.H., Hardy C.M., Kerr P.J.;
RT "The complete cDNA sequences of IL-2, IL-4, IL-6 and IL-10 from the
RT European rabbit (Oryctolagus cuniculus).";
RL Cytokine 12:555-565(2000).
DR EMBL; AF169168; AAF86652.1; -.
DR HSSP; P01585; 3INK.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
SQ SEQUENCE 133 AA; 14748 MW; 0D54758C190B5655 CRC64;

Query Match 64.7%; Score 99; DB 6; Length 133;
Best Local Similarity 69.0%; Pred. No. 5.6e-07;
Matches 20; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 APTSSSTKKTQLQLEHLLKLQMLNGIN 29
Db 21 APTSSSTKETQQLDLQLDLQLKGVN 49

RESULT 11
Q9UCF5 PRELIMINARY; PRT; 23 AA.
AC Q9UCF5;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DE Interleukin 2 precursor.
OS Cavia porcellus (Guinea pig).

DT 01-JUN-2000 (Tremblrel. 14, Last annotation update)
DE Interleukin 2 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RA MEDLINE=93289963; PubMed=8512072;
RX Mullner S., Karbe-Thonges B., Tripler D.;
RT "Charge heterogeneity of insulin fusion proteins expressed in
RT Escherichia coli is not due to proteolytic degradation.";
RL Anal. Biochem. 210:366-373(1993).
SQ SEQUENCE 23 AA; 2637 MW; 40B64C6875CE021F CRC64;

Query Match 54.9%; Score 84; DB 4; Length 23;
Best Local Similarity 85.7%; Pred. No. 1.7e-05;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 TSSSTKKTQLQLEHLLKLQML 23
Db 3 TSXSTKKTQLQLEHLLKLQML 23

RESULT 12
Q9XT84 PRELIMINARY; PRT; 154 AA.
AC Q9XT84;
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Interleukin 2.
OS Delphinapterus leucas (Beluga whale).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti;
OC Monodontidae; Delphinapterus.
OX NCBI_TaxID=9749;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99221046; PubMed=10206205;
RA St-Laurent G., Belliveau C., Archambault D.;
RT "Molecular cloning and phylogenetic analysis of beluga whale
RT (Delphinapterus leucas) and grey seal (Halichoerus grypus) interleukin
RL 2.";
RL Vet. Immunol. Immunopathol. 67:385-394(1999).
DR EMBL; AF072870; AAD40847.1; -.
DR HSSP; P01585; 3INK.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00265; INTERLEUKIN2.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
SQ SEQUENCE 154 AA; 17652 MW; 4288D3D41D04F172 CRC64;

Query Match 51.0%; Score 78; DB 6; Length 154;
Best Local Similarity 51.6%; Pred. No. 0.00087;
Matches 16; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

Qy 1 APTSSSTKKTQLQLEHLLKLQMLNGINNY 31
Db 21 APTSSSTENTKKVQSLLQLDLHLKLKINNH 51

RESULT 13
O88210 PRELIMINARY; PRT; 152 AA.
AC O88210;
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DT 01-OCT-2001 (Tremblrel. 18, Last annotation update)
DE Interleukin 2 precursor.
OS Cavia porcellus (Guinea pig).
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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 20, 2003, 10:04:02 ; Search time 19.1905 Seconds
(without alignments)
47.529 Million cell updates/sec

Title: US-09-776-781-8
Perfect score: 153
Sequence: 1 APTSSSTKTKQLQLEHLLKQMLNGINNY 31

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents:AA:*
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3: /cgn2.6/ptodata/1/1aa/6A_COMB.pep:*
4: /cgn2.6/ptodata/1/1aa/6B_COMB.pep:*
5: /cgn2.6/ptodata/1/1aa/PCTUS_COMB.pep:*
6: /cgn2.6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	147	96.1	50	1	US-08-127-351-13
2	147	96.1	50	1	US-08-480-3678-13
3	147	96.1	50	1	US-08-487-221A-13
4	147	96.1	50	1	US-08-480-370-13
5	147	96.1	88	4	US-08-817-787-15
6	147	96.1	96	1	US-08-160-376A-5
7	147	96.1	96	1	US-08-389-487-8
8	147	96.1	133	1	US-07-800-366-1
9	147	96.1	133	1	US-08-354-458A-5
10	147	96.1	133	1	US-08-225-224-3
11	147	96.1	133	1	US-08-318-193-89
12	147	96.1	133	1	US-08-284-393B-1
13	147	96.1	133	1	US-08-284-393B-2
14	147	96.1	133	1	US-08-284-393B-3
15	147	96.1	133	1	US-08-734-471-1
16	147	96.1	133	3	US-08-722-258-3
17	147	96.1	133	4	US-08-817-787-13
18	147	96.1	133	4	US-09-310-026-1
19	147	96.1	133	5	PCT-US95-04468-3
20	147	96.1	133	5	PCT-US95-08950-1
21	147	96.1	133	5	PCT-US95-08950-2
22	147	96.1	133	5	PCT-US95-08950-3
23	147	96.1	133	6	5210029-1
24	147	96.1	133	6	5256769-1
25	147	96.1	133	6	5464939-2
26	147	96.1	134	6	5496924-55
27	147	96.1	153	3	US-09-012-366-3

28	147	96.1	153	4	US-08-759-628-8	Sequence 8, Appl
29	147	96.1	153	4	US-09-522-217-111	Sequence 111, App
30	147	96.1	153	6	5314995-7	Patent No. 5314995
31	147	96.1	157	4	US-08-818-562-2	Sequence 2, Appl1
32	147	96.1	157	4	US-09-628-445-2	Sequence 2, Appl1
33	147	96.1	478	3	US-08-155-888-2	Sequence 2, Appl1
34	147	96.1	504	1	US-07-932-915-2	Sequence 2, Appl1
35	147	96.1	504	5	PCT-US91-05826-2	Sequence 2, Appl1
36	144	94.1	251	3	US-08-875-811-59	Sequence 59, Appl
37	144	94.1	254	3	US-08-875-811-61	Sequence 61, Appl
38	143	93.5	133	1	US-08-354-456A-6	Sequence 6, Appl1
39	140	91.5	31	4	US-09-116-594-2	Sequence 3, Appl1
40	132.5	86.6	127	3	US-08-806-121B-3	Sequence 3, Appl1
41	132.5	86.6	127	4	US-09-443-061-3	Sequence 3, Appl1
42	96	62.7	21	4	US-09-570-921-63	Sequence 63, Appl
43	96	62.7	21	4	US-09-570-921-68	Sequence 68, Appl
44	95	62.1	141	4	US-08-930-917A-18	Sequence 18, Appl
45	72	47.1	135	2	US-08-383-621-5	Sequence 5, Appl1

ALIGNMENTS

RESULT 1
US-08-127-351-13
; Sequence 13, Application US/08127351
; Patent No. 5449761
; GENERAL INFORMATION:
; APPLICANT: BELINKA JR, BENJAMIN A.
; APPLICANT: COUGHLIN, DANIEL J.
; APPLICANT: ALVAREZ, VERNON L.
; TITLE OF INVENTION: METAL-BINDING TARGETED POLYPEPTIDE
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER &
; ADDRESSEE: NEUSTADT,
; ADDRESS: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/127,351
; FILING DATE: 28-SEP-1993
; CLASSIFICATION: 534
; ATTORNEY/AGENT INFORMATION:
; NAME: Villacorta, Gilberto M.
; REGISTRATION NUMBER: 34,038
; REFERENCE/DOCKET NUMBER: 4980-004-44
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-127-351-13

Query Match 96.1%; Score 147; DB 1; Length 50;
Best Local Similarity 96.8%; Pred. No. 1.1e-15;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

APPLICATION NUMBER: US 08/127,351
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Villacorta, Gilberto M.
REGISTRATION NUMBER: 34,038
REFERENCE/DOCKET NUMBER: 4980-004-44
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-480-370-13

Query Match 96.1%; Score 147; DB 1; Length 50;
Best Local Similarity 96.8%; Pred. No. 1.1e-15;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 APTSSSTKKTQLQLEHLLKQLMILNGINNY 31
DB 1 APTSSSTKKTQLQLEHLLKQLMILNGINNY 31

RESULT 5
US-08-817-787-15
Sequence 15, Application US/08817787
Patent No. 6294353
GENERAL INFORMATION:
APPLICANT: Pack, Peter
APPLICANT: Lupas, Andrei
TITLE OF INVENTION: TARGETED HETERO-ASSOCIATION OF
RECOMBINANT PROTEINS TO MULTI-FUNCTIONAL COMPLEXES
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,787
FILING DATE: 23-SEP-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP95/04117
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94 11 6558.1
FILING DATE: 20-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 88 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-817-787-15

Query Match 96.1%; Score 147; DB 4; Length 88;
Best Local Similarity 96.8%; Pred. No. 2.2e-15;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 APTSSSTKKTQLQLEHLLKQLMILNGINNY 31
DB 3 APTSSSTKKTQLQLEHLLKQLMILNGINNY 33

RESULT 6
US-08-160-376A-5
Sequence 5, Application US/08160376A
Patent No. 5473049
GENERAL INFORMATION:
APPLICANT: Obermeier, Ranier
APPLICANT: Gerl, Martin
APPLICANT: Ludwig, Jurgen
APPLICANT: Sabel, Walter
TITLE OF INVENTION: Process For Obtaining Proinsulin
Possessing Correctly Linked
TITLE OF INVENTION: Cystine Bridges
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenneth A. Genoni, Esq.
STREET: Rt. 202-206 No. 5473049th/P.O. Box 2500
CITY: Somerville
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 08876-1258
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
COMPUTER: IBM 386
OPERATING SYSTEM: WINDOWS 3.1
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/160,376A
FILING DATE: December 1, 1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GE P 4240420.7
FILING DATE: December 2, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Barbara V. Maurer, Esq.
REGISTRATION NUMBER: 31,287
REFERENCE/DOCKET NUMBER: HOE 92/F 384
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 231-4079
TELEFAX: (908) 231-2255
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 96 Amino Acids
TYPE: Amino Acid (AA)
TOPOLOGY: not relevant
US-08-160-376A-5

Query Match 96.1%; Score 147; DB 1; Length 96;
Best Local Similarity 96.8%; Pred. No. 2.4e-15;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 APTSSSTKKTQLQLEHLLKQLMILNGINNY 31
DB 2 APTSSSTKKTQLQLEHLLKQLMILNGINNY 32

RESULT 7
US-08-389-487-8
Sequence 8, Application US/08389487
Patent No. 5663291
GENERAL INFORMATION:
APPLICANT: Obermeier, Ranier
APPLICANT: Gerl, Martin
APPLICANT: Ludwig, Jurgen

APPLICANT: Sabel, Walter
TITLE OF INVENTION: Process for Obtaining Insulin Having
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: United States of America
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/389,487
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Einaudi, Carol P.
REGISTRATION NUMBER: 32,220
REFERENCE/DOCKET NUMBER: 02481.1424-00000
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 96 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-389-487-8

Query Match 96.1%; Score 147; DB 1; Length 96;
Best Local Similarity 96.8%; Pred. No. 2.4e-15;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 APTSSSTKTKTQLQLEHLLKLQMLINGINNY 31
Db 2 APTSSSTKTKTQLQLEHLLKLQMLINGINNY 32

RESULT 8
US-07-800-366-1
Sequence 1, Application US/07800366
Patent No. 5250296
GENERAL INFORMATION:
APPLICANT: OOTSU, Koichiro
TITLE OF INVENTION: IMMUNOSTIMULANT AGENT CONTAINING
INTERLEUKIN-2 AND 5'-DEOXY-5-FLUOROURIDINE
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
ADDRESSEE: CUSHMAN
STREET: 130 Water Street
CITY: Boston
STATE: Massachusetts
COUNTRY: US
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/800,366
FILING DATE: 19911127
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:

NAME: Castle, Donald R
REGISTRATION NUMBER: 24,220
REFERENCE/DOCKET NUMBER: 41417(281)
TELEPHONE: (617)523-3400
TELEFAX: (617)523-3400
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 133 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-800-366-1

Query Match 96.1%; Score 147; DB 1; Length 133;

Best Local Similarity 96.8%; Pred. No. 3.6e-15;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 APTSSSTKTKTQLQLEHLLKLQMLINGINNY 31
Db 1 APTSSSTKTKTQLQLEHLLKLQMLINGINNY 31

RESULT 9

US-08-354-456A-5
Sequence 5, Application US/08354456A
Patent No. 5567611
GENERAL INFORMATION:
APPLICANT: Ralph, Peter
APPLICANT: Martin, George
APPLICANT: Platek, Michael
APPLICANT: Larrick, James W.
TITLE OF INVENTION: Multifunctional M-CSF Proteins and Genes Encoding
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHIRON CORPORATION
STREET: Intellectual Property - R440, P.O. Box 8097
CITY: Emeryville
STATE: California
COUNTRY: U.S.A.
ZIP: 94662-8097
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/354,456A
FILING DATE: 12-DEC-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/995,338
FILING DATE: 21-DEC-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McGarrigle Jr., Phillip L.
REGISTRATION NUMBER: 31,395
REFERENCE/DOCKET NUMBER: 750.003/32387
TELEPHONE: (510) 601-2718
TELEFAX: (510) 655-3542
TELEX: n/a
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 133 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-354-456A-5

Query Match 96.1%; Score 147; DB 1; Length 133;
Best Local Similarity 96.8%; Pred. No. 3.6e-15;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 APTSSSTKKTQLEHLLKQLMILGINNY 31
|||||
Db 1 APTSSSTKKTQLEHLLKQLMILGINNY 31

RESULT 10
US-08-225-224-3
; Sequence 3, Application US/08225224
; Patent No. 5635599
; GENERAL INFORMATION:
; APPLICANT: PASTAN, Ira
; APPLICANT: KREITMAN, Robert J.
; TITLE OF INVENTION: CIRCULARLY PERMUTATED LIGANDS AND
; TITLE OF INVENTION: CIRCULARLY PERMUTATED FUSION PROTEINS
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/225,224
; FILING DATE: 8-APR-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen L.
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 15280-193
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 133 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..133
; OTHER INFORMATION: /label= IL2
US-08-225-224-3

Query Match 96.1%; Score 147; DB 1; Length 133;
Best Local Similarity 96.8%; Pred. No. 3.6e-15;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 APTSSSTKKTQLEHLLKQLMILGINNY 31
|||||
Db 1 APTSSSTKKTQLEHLLKQLMILGINNY 31

RESULT 11
US-08-318-193-89
; Sequence 89, Application US/08318193
; Patent No. 5641663
; GENERAL INFORMATION:
; APPLICANT: GARVIN, Robert T.
; APPLICANT: MALEK, Lawrence T.
; TITLE OF INVENTION: AN EXPRESSION SYSTEM FOR THE SECRETION
; TITLE OF INVENTION: OF BIOACTIVE HUMAN GRANULOCYTE MACROPHAGE COLONY

; TITLE OF INVENTION: STIMULATING FACTOR (GM-CSF) AND OTHER HETEROLOGOUS
; TITLE OF INVENTION: PROTEINS FROM STREPTOMYCES
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,193
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,314
; FILING DATE:
; APPLICATION NUMBER: US 07/224,568
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 18740/116 CACO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 89:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 133 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-318-193-89

Query Match 96.1%; Score 147; DB 1; Length 133;
Best Local Similarity 96.8%; Pred. No. 3.6e-15;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 APTSSSTKKTQLEHLLKQLMILGINNY 31
|||||
Db 1 APTSSSTKKTQLEHLLKQLMILGINNY 31

RESULT 12
US-08-284-393B-1
; Sequence 1, Application US/08284393B
; Patent No. 5696234
; GENERAL INFORMATION:
; APPLICANT: Zurawski, Sandra M.
; APPLICANT: Zurawski, Gerard
; TITLE OF INVENTION: MUTAINS OF MAMMALIAN CYTOKINES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/284,393B
; FILING DATE: 01-AUG-1994
; CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0389
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-9196
TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 133 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-284-393B-1

Query Match 96.1%; Score 147; DB 1; Length 133;
Best Local Similarity 96.8%; Pred. No. 3.6e-15;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 APTSSSTKKTQLQLEHLLKQLMILNGINNY 31
|||||
Db 1 APTSSSTKKTQLQLEHLLKQLMILNGINNY 31

RESULT 13
US-08-284-393B-2
Sequence 2, Application US/08284393B
Patent No. 5696234
GENERAL INFORMATION:
APPLICANT: Zurawski, Sandra M.
APPLICANT: Zurawski, Gerard
TITLE OF INVENTION: MUTAINS OF MAMMALIAN CYTOKINES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/284,393B
FILING DATE: 01-AUG-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0389
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-9196
TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 133 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-284-393B-2

Query Match 96.1%; Score 147; DB 1; Length 133;
Best Local Similarity 96.8%; Pred. No. 3.6e-15;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 APTSSSTKKTQLQLEHLLKQLMILNGINNY 31
|||||
Db 1 APTSSSTKKTQLQLEHLLKQLMILNGINNY 31

RESULT 14
US-08-284-393B-3
Sequence 3, Application US/08284393B
Patent No. 5696234
GENERAL INFORMATION:
APPLICANT: Zurawski, Sandra M.
APPLICANT: Zurawski, Gerard
TITLE OF INVENTION: MUTAINS OF MAMMALIAN CYTOKINES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/284,393B
FILING DATE: 01-AUG-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0389
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-9196
TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 133 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-284-393B-3

Query Match 96.1%; Score 147; DB 1; Length 133;
Best Local Similarity 96.8%; Pred. No. 3.6e-15;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 APTSSSTKKTQLQLEHLLKQLMILNGINNY 31
|||||
Db 1 APTSSSTKKTQLQLEHLLKQLMILNGINNY 31

RESULT 15
US-08-734-471-1
Sequence 1, Application US/08734471
Patent No. 5800810
GENERAL INFORMATION:
APPLICANT: Doyle, Michael V.
APPLICANT: Newell, Arthur D.
APPLICANT: Nunberg, Jack H.
APPLICANT: White, Thomas J.
TITLE OF INVENTION: HUMAN IL-2 AS A VACCINE ADJUVANT
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation, Intellectual Property R440
STREET: P O Box 8097
CITY: Emeryville
STATE: California
COUNTRY: United States of America
ZIP: 94662-8097
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

Search completed: February 20, 2003, 10:08:11
Job time : 20.1905 secs

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US-09-766-543-14

Query Match 93.5%; Score 143; DB 10; Length 133;
Best Local Similarity 96.7%; Pred. No. 1e-14;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PTSSSTKKTQLQLEHLLKLQMLNGINNY 31
DB 2 PTSSSTKKTQLQLEHLLKLQMLNGINNY 31

RESULT 7

US-09-033-525-2
; Sequence 2, Application US/09033525
; Patent No. US20020090374A1
; GENERAL INFORMATION:
; APPLICANT: Yarkoni, Shai
; APPLICANT: Ben-Yehudah, Ahmi
; APPLICANT: Azar, Yehudith
; APPLICANT: Agellan, Rami
; APPLICANT: Belotsotsky, Ruth
; APPLICANT: Lorberdoun-Galski, Haya
; TITLE OF INVENTION: CHIMERIC PROTEINS WITH CELL-TARGETING
; FILE REFERENCE: 9457-009-999
; CURRENT APPLICATION NUMBER: US/09/033,525
; CURRENT FILING DATE: 1998-03-02
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-033-525-2

Query Match 93.5%; Score 143; DB 10; Length 331;
Best Local Similarity 96.7%; Pred. No. 3.1e-14;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PTSSSTKKTQLQLEHLLKLQMLNGINNY 31
DB 4 PTSSSTKKTQLQLEHLLKLQMLNGINNY 33

RESULT 8

US-09-835-147-11
; Sequence 11, Application US/09835147
; Patent No. US20020002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
US-09-835-147-11

; OTHER INFORMATION: construct of human CD39
US-09-835-147-11

Query Match 37.3%; Score 57; DB 10; Length 43;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APTSSSTKKTQL 12
DB 25 APTSSSTKKTQL 36

RESULT 9

US-09-835-147-6
; Sequence 6, Application US/09835147
; Patent No. US20020002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
US-09-835-147-6

Query Match 37.3%; Score 57; DB 10; Length 454;
Best Local Similarity 100.0%; Pred. No. 0.54;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APTSSSTKKTQL 12
DB 1 APTSSSTKKTQL 12

RESULT 10

US-09-835-147-8
; Sequence 8, Application US/09835147
; Patent No. US20020002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
US-09-835-147-8

RESULT 14
 US-10-142-120-1
 ; Sequence 1, Application US/10142120
 ; Patent No. US20020164302A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Epostein, Alan L.
 ; TITLE OF INVENTION: VASOPERMABILITY ENHANCING PEPTIDE FRAGMENT OF HUMAN INTERLEUKIN-
 ; FILE REFERENCE: 1920-325D2-09801297
 ; CURRENT APPLICATION NUMBER: US/10/142,120
 ; CURRENT FILING DATE: 2002-05-09
 ; PRIOR APPLICATION NUMBER: 09/443,061
 ; PRIOR FILING DATE: 1999-11-18
 ; PRIOR APPLICATION NUMBER: 08/806,121
 ; PRIOR FILING DATE: 1996-12-23
 ; NUMBER OF SEQ ID NOS: 2
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 1
 ; LENGTH: 37
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-142-120-1

Query Match 32.7%; Score 50; DB 9; Length 37;
 Best Local Similarity 90.0%; Pred. No. 0.3;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 22 OMILINGINNY 31
 :|||||
 Db 1 EMILINGINNY 10

RESULT 15
 US-09-796-149-5
 ; Sequence 5, Application US/09796149
 ; Patent No. US20020035079A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Univ. of Southern California
 ; TITLE OF INVENTION: Mutated cyclin G1 protein
 ; FILE REFERENCE: 4-31342A/USC
 ; CURRENT APPLICATION NUMBER: US/09/796,149
 ; CURRENT FILING DATE: 2001-02-28
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 5
 ; LENGTH: 226
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-796-149-5

Query Match 30.7%; Score 47; DB 10; Length 226;
 Best Local Similarity 60.0%; Pred. No. 7.6;
 Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 7 TKKTQLQLEHLLKL 21
 :|||:|:|:|:|:
 Db 82 TKKQVLMEHLVLKV 96

Search completed: February 20, 2003, 10:08:33
 Job time : 8.87302 secs

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